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(54) Title: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

(57) Abstract: Peptide sequences capable of binding to insulin and/or insulin-like growth factor receptors with either agonist or antagonist activity and identified from various peptide libraries are disclosed. This invention also identifies at least two different binding sites, which are present on insulin and insulin-like growth factor receptors, and which selectively bind the peptides of this invention. As agonists, certain of the peptides of this invention may be useful for development as therapeutics to supplement or replace endogenous peptide hormones. The antagonists may also be developed as therapeutics.



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INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS

This application is a continuation-in-part of U.S. Application Serial No. 09/538,038 filed September 24, 2002, which is a continuation-in-part of U.S. Application Serial No. 09/538,038 filed March 29, 2000, which is a continuation-in-part of U.S. Application Serial No. 09/146,127, filed September 2, 1998, both of which are incorporated by reference in their entirety.

I. FIELD OF THE INVENTION

This invention relates to the field of hormone receptor activation or inhibition. More specifically, this invention relates to the identification of molecular structures, especially peptides, which are capable of acting at either the insulin or insulin-like growth factor receptors as agonists or antagonists. Also related to this invention is the field of molecular modeling whereby useful molecular models are derived from known structures.

II. BACKGROUND OF THE INVENTION

Insulin is a potent metabolic and growth promoting hormone that acts on cells to stimulate glucose, protein, and lipid metabolism, as well as RNA and DNA synthesis. A well-known effect of insulin is the regulation of glucose levels in the body. This effect occurs predominantly in liver, fat, and muscle tissue. In the liver, insulin stimulates glucose incorporation into glycogen and inhibits the production of glucose. In muscle and fat tissue, insulin stimulates glucose uptake, storage, and metabolism. Defects in glucose utilization are very common in the population, giving rise to diabetes.

Insulin initiates signal transduction in target cells by binding to a specific cell-surface receptor, the insulin receptor (IR). The binding leads to conformational changes in the extracellular domain of IR, which are transmitted across the cell membrane and result in activation of the

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receptor's tyrosine kinase activity. This, in turn, leads to autophosphorylation of tyrosine kinase of IR, and the binding of soluble effector molecules that contain SH2 domains such as phosphoinositol-3-kinase, Ras GTPase-activating protein, and phospholipase C γ to IR (Lee and Pilch, 1994, *Am. J. Physiol.* **266**:C319-C334).

Insulin-like growth factor 1 (IGF-1) is a small, single-chain protein (MW = 7,500 Da) that is involved in many aspects of tissue growth and repair. Recently, IGF-1 has been implicated in various forms cancer including prostate, breast, colorectal, and ovarian cancers. It is similar in size, sequence, and structure to insulin, but has 100-1,000-fold lower affinity for IR (Mynarcik *et al.*, 1997, *J. Biol. Chem.* **272**:18650-18655).

Clinically, recombinant human IGF-1 has been investigated for the treatment of several diseases, including type I diabetes (Carroll *et al.*, 1997, *Diabetes* **46**:1453-1458; Crowne *et al.*, 1998, *Metabolism* **47**:31-38), amyotrophic lateral sclerosis (Lai *et al.*, 1997, *Neurology* **49**:1621-1630), and diabetic motor neuropathy (Apfel and Kessler, 1996, *CIBA Found. Symp.* **196**:98-108). Other potential therapeutic applications of IGF-1, such as osteoporosis (Canalis, 1997, *Bone* **21**:215-216), immune modulation (Clark, 1997, *Endocr. Rev.* **18**:157-179) and nephrotic syndrome (Feld and Hirshberg, 1996, *Pediatr. Nephrol.* **10**:355-358), are also under investigation.

A number of studies have analyzed the role of endogenous IGF-1 in various disease states. Interestingly, several reports have shown that IGF-1 promotes the growth of normal and cancerous prostate cells both *in vitro* and *in vivo* (Angelloz-Nicoud and Binoux, 1995, *Endocrinol.* **136**:5485-5492; Figueroa *et al.*, 1995, *J. Clin. Endocrinol. Metab.* **80**:3476-3482; Topping *et al.*, 1997, *J. Urol.* **158**:222-227). Additionally, elevated serum IGF-1 levels correlate with increased risks of prostate cancer, and may be an earlier predictor of cancer than is prostate-specific antigen (PSA) (Chan *et al.*, 1998, *Science* **279**:563-566). Recent studies have indicated a connection between IGF-1 levels and other cancers such as breast, colorectal, and

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ovarian. Serum IGF-1 levels are regulated by the presence of IGF binding proteins (IGFBP) which bind to IGF-1 and prevent its interaction with the IGF-1 receptor (IGF-1R; reviewed in Conover, 1996, *Endocr. J.* **43S**:S43-S48 and Rajaram *et al.*, 1997, *Endocr. Rev.* **18**:801-831). Interestingly, PSA
5 has been shown to be a protease that cleaves IGFBP-3, resulting in an increase of free IGF-1 in serum (Cohen *et al.*, 1992, *J. Clin. Endocrinol. Metab.* **75**:1046-1053; Cohen *et al.*, 1994, *J. Endocrinol.* **142**:407-415; Lilja, 1995, *J. Clin. Lab. Invest. Suppl.* **220**:47-56). Clearly, regulation of IGF-1R activity can play an important role in several disease states, indicating that
10 there are potential clinical applications for both IGF-1 agonists and antagonists.

IGF-1R and IR are related members of the tyrosine-kinase receptor superfamily of growth factor receptors. Both types of receptors are composed of two α and two β subunits which form a disulfide-linked
15 heterotetramer (β - α - α - β). These receptors have an extracellular ligand binding domain, a single transmembrane domain, and a cytoplasmic domain displaying the tyrosine kinase activity. The extracellular domain is composed of the entire α subunits and a portion of the N-terminus of the β subunits, while the intracellular portion of the β subunits contains the
20 tyrosine kinase domain. Another family member is insulin-related receptor (IRR), for which no natural ligand is known.

While similar in structure, IGF-1R and IR serve different physiological functions. IR is primarily involved in metabolic functions whereas IGF-1R mediates growth and differentiation. However, both insulin and IGF-1 can
25 induce both mitogenic and metabolic effects. Whether each ligand elicits both activities via its own receptor, or whether insulin exerts its mitogenic effects through its weak affinity binding to IGF-1R, and IGF-1 its metabolic effects through IR, remains controversial (De Meyts, 1994, *Horm. Res.* **42**:152-169).

30 IR is a glycoprotein having molecular weight of 350-400 kDa (depending of the level of glycosylation). It is synthesized as a single

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polypeptide chain and proteolytically cleaved to yield a disulfide-linked monomer α - β insulin receptor. Two α - β monomers are linked by disulfide bonds between the α -subunits to form a dimeric form of the receptor (β - α - α - β -type configuration). The α subunit is comprised of 723 amino acids, and it
5 can be divided into two large homologous domains, L1 (amino acids 1-155) and L2 (amino acids 313-468), separated by a cysteine rich region (amino acids 156-312) (Ward *et al.*, 1995, *Prot. Struct. Funct. Genet.* **22**:141-153). Many determinants of insulin binding seem to reside in the α -subunit. A unique feature of IR is that it is dimeric in the absence of ligand.

10 The sequence of IR is highly homologous to the sequence of IGF-1R. The sequence identity level varies from about 40% to 70%, depending on the position within the α -subunit. The three-dimensional structures of both receptors may therefore be similar. The crystal structure of the first three domains of IGF-1R has been determined (Garrett *et al.*, 1998, *Nature*
15 **394**:395-399). The L domains consist of a single-stranded right-handed β -helix (a helical arrangement of β -strands), while the cysteine-rich region is composed of eight disulfide-bonded modules.

The β -subunit of the insulin receptor has 620 amino acid residues and three domains: extracellular, transmembrane, and cytosolic. The
20 extracellular domain is linked by disulfide bridges to the α -subunit. The cytosolic domain includes the tyrosine kinase domain, the three-dimensional structure of which has been solved (Hubbard *et al.*, 1994, *Nature* **372**:746-754).

To aid in drug discovery efforts, a soluble form of a membrane-bound
25 receptor was constructed by replacing the transmembrane domain and the intracellular domain of IR with constant domains from immunoglobulin Fc or λ subunits (Bass *et al.*, 1996, *J. Biol. Chem.* **271**:19367-19375). The recombinant gene was expressed in human embryonic kidney 293 cells. The expressed protein was a fully processed heterotetramer and the ability
30 to bind insulin was similar to that of the full-length holoreceptor.

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IGF-1 and insulin competitively cross-react with IGF-1R and IR. (L. Schäffer, 1994, *Eur. J. Biochem.* **221**:1127-1132). Despite 45% overall amino acid identity, insulin and IGF-1 bind only weakly to each other's receptor. The affinity of each peptide for the non-cognate receptor is about
5 3 orders of magnitude lower than that for the cognate receptor (Mynarcik, *et al.*, 1997, *J. Biol. Chem.* **272**:18650-18655). The differences in binding affinities may be partly explained by the differences in amino acids and unique domains which contribute to unique tertiary structures of ligands (Blakesley *et al.*, 1996, *Cytokine Growth Factor Rev.* **7**(2):153-9).

10 Both insulin and IGF-1 are expressed as precursor proteins comprising, among other regions, contiguous A, B, and C peptide regions, with the C peptide being an intervening peptide connecting the A and B peptides. A mature insulin molecule is composed of the A and B chains connected by disulfide bonds, where the connecting C peptide has been
15 removed during post-translational processing. IGF-1 retains its smaller C-peptide as well as a small D extension at the C-terminal end of the A chain, making the mature IGF-1 slightly larger than insulin (Blakesley, 1996). The C region of human IGF-1 appears to be required for high affinity binding to IGF-1R (Pietrzkowski *et al.*, 1992, *Cancer Res.* **52**(23):6447-51).
20 Specifically, tyrosine 31 located within this region appears to be essential for high affinity binding. Furthermore, deletion of the D domain of IGF-1 increased the affinity of the mutant IGF-1 for binding to the IR, while decreasing its affinity for the IGF-1R (Pietrzkowski *et al.*, 1992). A further distinction between the two hormones is that, unlike insulin, IGF-1 has very
25 weak self-association and does not hexamerize (De Meyts, 1994).

The α -subunits, which contain the ligand binding region of IR and IGF-1R, demonstrate between 47-67% overall amino acid identity. Three general domains have been reported for both receptors from sequence analysis of the α subunits, L1-Cys-rich-L2. The cysteine residues in the C-rich region are highly conserved between the two receptors; however, the
30 cysteine-rich domains have only 48% overall amino acid identity.

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Despite the similarities observed between these two receptors, the role of the domains in specific ligand binding are distinct. Through chimeric receptor studies, (domain swapping of the IR and IGF-1R α -subunits), researchers have reported that the sites of interaction of the ligands with their specific receptors differ (T. Kjeldsen *et al.*, 1991, *Proc. Natl. Acad. Sci. USA* **88**:4404-4408; A.S. Andersen *et al.*, 1992, *J. Biol. Chem.* **267**:13681-13686). For example, the cysteine-rich domain of the IGF-1R was determined to be essential for high-affinity IGF binding, but not insulin binding. When amino acids 191-290 of IGF-1R region was introduced into the corresponding region of the IR (amino acids 198-300), the modified IR bound both IGF-1 and insulin with high affinity. Conversely, when the corresponding region of the IR was introduced into the IGF-1R, the modified IGF-1R bound to IR but not IGF-1.

A further distinction between the binding regions of the IR and IGF-1R is their differing dependence on the N-terminal and C-terminal regions. Both the N-terminal and C-terminal regions (located within the putative L1 and L2 domains) of the IR are important for high-affinity insulin binding but appear to have little effect on IGF-1 binding for either IR or IGF-1R. Replacing residues in the N-terminus of IGF-1R (amino acids 1-62) with the corresponding residues of IR (amino acids 1-68) confers insulin-binding ability on IGF-1R. Within this region, residues Phe-39, Arg-41 and Pro-42 are reported as major contributors to the interaction with insulin (Williams *et al.*, 1995). When these residues are introduced into the equivalent site of IGF-1R, the affinity for insulin is markedly increased, whereas, substitution of these residues by alanine in IR results in markedly decreased insulin affinity. Similarly, the region between amino acids 704-717 of the C-terminus of IR has been shown to play a major role in insulin specificity. Substitution of these residues with alanine also disrupts insulin binding (Mynarcik *et al.*, 1996, *J. Biol. Chem.* **271**(5):2439-42; C. Kristensen *et al.*, 1999, *J. Biol. Chem.* **274**(52):37351-37356).

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Further studies of alanine scanning of the receptors suggest that insulin and IGF-1 may use some common contacts to bind to IGF-1R but that those contacts differ from those that insulin utilizes to bind to IR (Mynarcik *et al.*, 1997). Hence, the data in the literature has led one
5 commentator to state that even though "the binding interfaces for insulin and IGF-1 on their respective receptors may be homologous within this interface the side chains which make actual contact and determine specificity may be quite different between the two ligand-receptor systems" (De Meyts, 1994).

Based on data for binding of insulin and insulin analogs to various
10 insulin receptor constructs, a binding model has been proposed. This model shows insulin receptor with two insulin binding sites that are positioned on two different surfaces of the receptor molecule, such that each alpha-subunit is involved in insulin binding. In this way, activation of the insulin receptor is believed to involve cross-connection of the alpha-subunits by insulin. A
15 similar mechanism may operate for IGF-1R, but one of the receptor binding interactions appears to be different (Schäffer, 1994, *Eur. J. Biochem.* **221**:1127-1132).

The identification of molecular structures having a high degree of specificity for one or the other receptor is important to developing efficacious
20 and safe therapeutics. For example, a molecule developed as an insulin agonist should have little or no IGF-1 activity in order to avoid the mitogenic activity of IGF-1 and a potential for facilitating neoplastic growth. It is therefore important to determine whether insulin and IGF-1 share common three-dimensional structures but which have sufficient differences to confer
25 selectivity for their respective receptors. Similarly, it would be desirable to identify other molecular structures that mimic the active binding regions of insulin and/or IGF-1 and which impart selective agonist or antagonist activity.

Although certain proteins are important drugs, their use as
30 therapeutics presents several difficult problems, including the high cost of production and formulation, administration usually via injection and limited

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stability in the bloodstream. Therefore, replacing proteins, including insulin or IGF-1, with small molecular weight drugs has received much attention. However, to date, none of these efforts has resulted in finding an effective drug replacement.

5 Peptides mimicking functions of protein hormones have been previously reported. Yanofsky *et al.* (1996, *Proc. Natl. Acad. Sci. USA* 93:7381-7386) reported the isolation of a monomer antagonistic to IL-1 with nanomolar affinity for the IL-1 receptor. This effort required construction and use of many phage displayed peptide libraries and sophisticated phage-
10 panning procedures.

 Wrighton *et al.* (1996, *Science* **273**:458-464) and Livnah *et al.* (1996, *Science* **273**:464-471) reported dimer peptides that bind to the erythropoietin (EPO) receptor with full agonistic activity *in vivo*. These peptides are cyclical and have intra-peptide disulfide bonds; like the IL-1 receptor
15 antagonist, they show no significant sequence identity to the natural ligand. Importantly, X-ray crystallography revealed that it was the spontaneous formation of non-covalent peptide homodimer peptides that enabled the dimerization two EPO receptors.

 WO 96/04557 reported the identification of peptides and antibodies
20 that bound to active sites of biological targets, which were subsequently used in competition assays to identify small molecules that acted as agonist or antagonists at the biological targets. Renchler *et al.* (1994, *Proc. Natl. Acad. Sci. USA* **91**:3623-3627) reported synthetic peptide ligands of the antigen binding receptor that induced programmed cell death in human B-
25 cell lymphoma.

 Most recently, Cwirla *et al.* (1997, *Science* **276**:1696-1698) reported the identification of two families of peptides that bound to the human thrombopoietin (TPO) receptor and were competed by the binding of the natural TPO ligand. The peptide with the highest affinity, when dimerized by
30 chemical means proved to be as potent an *in vivo* agonist as TPO, the natural ligand.

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III. SUMMARY OF THE INVENTION

This invention relates to the identification of amino acid sequences that specifically recognize sites involved in IR or IGF-1R activation. Specific amino acid sequences are identified and their agonist or antagonist activity at IR and/or IGF-1R has been determined. Such sequences may be developed as potential therapeutics or as lead compounds to develop other more efficacious ones. In addition, these sequences may be used in high-throughput screens to identify and provide information on small molecules that bind at these sites and mimic or antagonize the functions of insulin or IGF-1. Furthermore, the peptide sequences provided by this invention can be used to design secondary peptide libraries, which can be used to identify sequence variants that increase or modulate the binding and/or activity of the original peptide at IR or IGF-1R.

In one aspect of this invention, large numbers of peptides have been screened for their IR and IGF-1R binding and activity characteristics. Analysis of their amino acid sequences has identified certain consensus sequences which may be used themselves or as core sequences in larger amino acid sequences conferring upon them agonist or antagonist activity. Several generic amino acid sequences are disclosed which bind IR and/or IGF-1R with varying degrees of agonist or antagonist activity depending on the specific sequence of the various peptides identified within each motif group. Also provided are amino or carboxyl terminal extensions capable of modifying the affinity and/or pharmacological activity of the consensus sequences when part of a larger amino acid sequence.

The amino acid sequences of this invention which bind IR and/or IGF-1R include:

- a. $X_1 X_2 X_3 X_4 X_5$ wherein X_1 , X_2 , X_4 and X_5 are aromatic amino acids, and X_3 is any polar amino acid (Formula 1; Group 1; A6 motif);
- b. $X_6 X_7 X_8 X_9 X_{10} X_{11} X_{12} X_{13}$ wherein X_6 and X_7 are aromatic amino acids, X_8 , X_9 , X_{11} and X_{12} are any amino acid, and X_{10} and X_{13} are hydrophobic amino acids (Formula 2; Group 3; B6 motif);

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c. $X_{14} X_{15} X_{16} X_{17} X_{18} X_{19} X_{20} X_{21}$ wherein X_{14} , and X_{17} are hydrophobic amino acids, X_{15} , X_{16} , X_{18} and X_{19} are any amino acid, and X_{20} and X_{21} are aromatic amino acids (Formula 3; reverse B6; revB6).

d. $X_{22} X_{23} X_{24} X_{25} X_{26} X_{27} X_{28} X_{29} X_{30} X_{31} X_{32} X_{33} X_{34} X_{35} X_{36} X_{37} X_{38}$
 5 $X_{39} X_{40} X_{41}$ wherein X_{22} , X_{25} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{36} , X_{37} , X_{38} , X_{40} , and X_{41} are any amino acid, X_{35} and X_{37} may be any amino acid for binding to IR, whereas X_{35} is preferably a hydrophobic amino acid and X_{37} is preferably glycine for binding to IGF-1R and possess agonist or antagonist activity. X_{23} and X_{26} are hydrophobic amino acids. This sequence further comprises at
 10 least two cysteine residues, preferably at X_{25} and X_{40} X_{31} and X_{32} are small amino acids (Formula 4; Group 7; E8 motif).

e. $X_{42} X_{43} X_{44} X_{45} X_{46} X_{47} X_{48} X_{49} X_{50} X_{51} X_{52} X_{53} X_{54} X_{55} X_{56} X_{57} X_{58}$
 $X_{59} X_{60} X_{61}$ wherein X_{42} , X_{43} , X_{44} , X_{45} , X_{53} , X_{55} , X_{56} , X_{58} , X_{60} and X_{61} may be any amino acid, X_{43} , X_{46} , X_{49} , X_{50} , X_{54} are hydrophobic amino acids, X_{47} and
 15 X_{59} are preferably cysteines, X_{48} is a polar amino acid, and X_{51} , X_{52} and X_{57} are small amino acids (Formula 5; mini F8 motif).

f. $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78}$
 $X_{79} X_{80} X_{81}$ wherein X_{62} , X_{65} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} , and X_{81} may be any amino acid; X_{63} , X_{70} , X_{74} are hydrophobic amino acids; X_{64} is a polar
 20 amino acid, X_{67} and X_{75} are aromatic amino acids and X_{72} and X_{79} are preferably cysteines capable of forming a loop (Formula 6; Group 2; D8 motif).

g. $H X_{82} X_{83} X_{84} X_{85} X_{86} X_{87} X_{88} X_{89} X_{90} X_{91} X_{92}$ wherein X_{82} is proline or alanine, X_{83} is a small amino acid, X_{84} is selected from leucine,
 25 serine or threonine, X_{85} is a polar amino acid, X_{86} , X_{88} , X_{89} and X_{90} are any amino acid, and X_{87} , X_{91} and X_{92} are an aliphatic amino acid (Formula 7).

h. $X_{104} X_{105} X_{106} X_{107} X_{108} X_{109} X_{110} X_{111} X_{112} X_{113} X_{114}$ wherein at least one of the amino acids of X_{106} through X_{111} , and preferably two, are tryptophan separated by three amino acids, and wherein at least one of X_{104} ,
 30 X_{105} and X_{106} and at least one of X_{112} , X_{113} and X_{114} are cysteine (Formula 8); and

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i. an amino acid sequence comprising the sequence JBA5: DYKDLCQSWGVRIGWLAGLCPKK (SEQ ID NO:1541) or JBA5 minus FLAG® tag and terminal lysines: LCQSWGVRIGWLAGLCP (SEQ ID NO:1542) (Formula 9).

5 j. $W X_{123} G Y X_{124} W X_{125} X_{126}$ (SEQ ID NO:1543) wherein X_{123} is selected from proline, glycine, serine, arginine, alanine or leucine, but more preferably proline; X_{124} is any amino acid, but preferably a charged or aromatic amino acid; X_{125} is a hydrophobic amino acid preferably leucine or phenylalanine, and most preferably leucine. X_{126} is any amino acid, but
10 preferably a small amino acid (Formula 10; Group 6 motif).

In one embodiment, peptides comprising a preferred amino acid sequence FYX_3WF (SEQ ID NO: 1544) (Formula 1; Group 1; A6 motif) have been identified which competitively bind to sites on IR. Surprisingly, peptides comprising an amino acid sequence FYX_3WF (SEQ ID NO:1544)
15 can possess agonist or antagonist activity at IR.

This invention also identifies at least two distinct binding sites on IR based on the differing ability of certain of the peptides to compete with one another and insulin for binding to IR. Accordingly, this invention provides amino acid sequences that bind specifically to one or both sites of IR.
20 Furthermore, specific amino acid sequences are provided which have either agonist or antagonist characteristics based on their ability to bind to the specific sites of IR.

In another embodiment of this invention, amino acid sequences which bind to one or more sites of IR or IGF-1R (e.g., Site 1 or Site 2) are
25 covalently linked together to form multivalent ligands. These multivalent ligands are capable of forming complexes with a plurality of IR or IGF-1R. Either the same or different amino acid sequences are covalently bound together to form homo- or heterocomplexes.

In various aspects of the invention, monomer subunits are covalently
30 linked at their N-termini or C-termini to form N-N, C-C, N-C, or C-N linked dimer peptides. In one example, dimer peptides are used to form receptor

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complexes bound through the same corresponding sites, e.g., Site 1-Site 1 or Site 2-Site 2 dimers. Alternatively, heterodimer peptides are used to bind to different sites on one receptor or to cause receptor complexing through different sites, e.g., Site 1-Site 2 or Site 2-Site 1 dimers. In one novel aspect
5 of the invention, Site 2-Site 1 dimers find use as insulin agonists, while certain Site 1-Site 2 dimers find use as insulin antagonists.

In various embodiments, insulin agonists comprise Site 1-Site 1 dimer peptide sequences S325, S332, S333, S335, S337, S353, S374-S376, S378, S379, S381, S414, S415, and S418; whereas other insulin agonists
10 comprise Site 2-Site 1 dimer peptide sequences S455, S457, S458, S467, S468, S471, S499, S510, S518, S519, and S520, as described herein below. In one preferred embodiment, an insulin agonist comprises the sequence of the S519 dimer peptide, which shows insulin-like activity in both *in vitro* and *in vivo* assays.

15 The present invention also provides assays for identifying compounds that mimic the binding characteristics of insulin or IGF-1. Such compounds may act as antagonists or agonists of insulin or IGF-1 function in cell based assays.

This invention further provides kits for identifying compounds that
20 bind to IR and/or IGF-1R. Also provided are therapeutic compounds that bind the insulin receptor or the IGF-1 receptor.

Other embodiments of this invention are the nucleic acid sequences encoding the amino acid sequences of the invention. Also within the scope of this invention are vectors containing the nucleic acids and host cells
25 which express the nucleic acids encoding the amino acid sequences which bind at IR and/or IGF-1R and possess agonist or antagonist activity.

This invention also provides amino acid sequences that bind to active sites of IR and/or IGF-1R and to identify structural criteria for conferring agonist or antagonist activity at IR or IGF-1R.

30 This invention further provides specific amino acid sequences that possess agonist, partial agonist, or antagonist activity at either IR or IGF-1R.

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Such amino acid sequences are potentially useful as therapeutics themselves or may be used to identify other molecules, especially small organic molecules, which possess agonist or antagonist activity at IR or IGF-1R.

5 In addition, the present invention provides structural information derived from the amino acid sequences of this invention, which may be used to construct other molecules possessing the desired activity at the relevant IR binding site.

IV. **BRIEF DESCRIPTION OF THE DRAWINGS**

10 Figures 1A-1O; 2A-2E; 3A-3E; 4A-4I; 43A-43B, 44A-44B: Amino acid sequences identified by panning peptide libraries against IGF-1R and/or IR. The amino acids are represented by their one-letter abbreviation. The ratios over background are determined by dividing the signal at 405 nm (E-Tag, IGF-1R, or IR) by the signal at 405 nm for non-fat milk. The IGF-1R/IR Ratio
15 Comparison is determined by dividing the ratio of IGF-1R by the ratio of IR. The IR/IGF-1R Ratio Comparison is determined by dividing the ratio of IR by the ratio of IGF-1R. HIT indicates binder; CAND indicates binder candidate; LDH indicates binding to lactate dehydrogenase (negative control); Sp/Irr indicates the ratio of specific binding over non-specific binding.

20 The design of each library is shown in the first line in bold. In the design, symbol 'X' indicates a random position, an underlined amino acid indicates a doped position at the nucleotide level, and other positions are held constant. Additional abbreviations in the B6H library are: 'O' indicates an NGY codon where Y is C or T; 'J' indicates an RHR codon where R is A or G, and H is A, C, or T; and 'U' indicates an VVY codon where V is A, C, or
25 G, and Y is C or T. The 'h' in the 20E2 libraries indicates an NTN codon.

 Symbols in the listed sequences are: Q - TAG Stop; # -TAA Stop; * - TGA Stop; and ? - Unknown Amino Acid. It is believed that a W replaces the TGA Stop Codon when expressed. Except for the 20C and A6L
30 libraries, all libraries are designed with the short FLAG® Epitope DYKD

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(SEQ ID NO:1545; Hopp *et al.*, 1988, *Bio/Technology* 6:1205-1210) at the N-terminus of the listed sequence and AAAGAP (SEQ ID NO:1546) at the C-terminus. The 20C and A6L libraries have the full length FLAG® epitope DYKDDDDK (SEQ ID NO:1547).

5 Figure 1A: Formula 1 motif peptide sequences obtained from a random 40mer library panned against IR (SEQ ID NOS:1-3).

 Figure 1B: Formula 1 motif peptide sequence obtained from a random 40mer library panned against IGF-1R (SEQ ID NOS:4-6).

 Figure 1C: Formula 1 motif peptide sequences obtained from a
10 random 20mer library panned against IR (SEQ ID NOS:7-29).

 Figure 1D: Formula 1 motif peptide sequences obtained from a random 20mer library panned against IGF-1R (SEQ ID NOS:30-33).

 Figure 1E: Formula 1 motif peptide sequences obtained from a 21mer library constructed to contain $X_{1-10}NFYDWFVX_{18-21}$ (SEQ ID NO:34; also referred to as "A6S") panned against IR (SEQ ID NOS:35-98).
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 Figure 1F: Formula 1 motif peptide sequences obtained from a 21mer library constructed to contain $X_{1-10}NFYDWFVX_{18-21}$ (SEQ ID NO:34; also referred to as "A6S") panned against IGF-1R (SEQ ID NOS:99-166).

 Figure 1G: Formula 1 motif peptide sequences obtained from a
20 library constructed to contain variations outside the consensus core of the A6 peptide as indicated (referred to as "A6L" (SEQ ID NO: 167)) panned against IR (SEQ ID NOS:168-216).

 Figure 1H: Formula 1 motif peptide sequences obtained from a library constructed to contain variations outside the consensus core of the
25 A6 peptide as indicated (referred to as "A6L" (SEQ ID NO: 167)) panned against IGF-1R (SEQ ID NOS:217-244).

 Figure 1I: Formula 1 motif peptide sequences obtained from a library constructed to contain variations in the consensus core of the E4D peptide (SEQ ID NO: 245) (as indicated) panned against IR (SEQ ID
30 NOS:246-305).

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Figure 1J: Formula 1 motif peptide sequences obtained from a library constructed to contain variations in the consensus core of the E4D peptide (SEQ ID NO: 245) (as indicated) panned against IGF-1R (SEQ ID NOS:306-342).

5 Figure 1K: Formula 1 motif peptide sequences obtained from a library constructed using the sequence $X_{1-6}FHENFYDWFVRQVSX_{21-26}$ (SEQ ID NO:343; H2C-A) panned against IR (SEQ ID NOS:344-430).

Figure 1L: Formula 1 motif peptide sequences obtained from a library constructed using the sequence $X_{1-6}FHENFYDWFVRQVSX_{21-26}$ (SEQ ID NO:343; H2C-A) panned against IGF-1R (SEQ ID NOS:431-467).

10 Figure 1M: Formula 1 motif peptide sequences obtained from a library constructed using the sequence $X_{1-6}FHXXFYXWFX_{16-21}$ (SEQ ID NO:468; H2C-B) and panned against IR (SEQ ID NOS:469-575).

Figure 1N: Formula 1 motif peptide sequences obtained from a library constructed using the sequence $X_{1-6}FHXXFYXWFX_{16-21}$ (SEQ ID NO:468; H2C-B) and panned against IGF-1R (SEQ ID NOS:576-657).

Figure 1O: Formula 1 motif peptide sequences obtained from other libraries panned against IR (SEQ ID NOS:658-712).

Figure 2A: Formula 4 motif peptide sequences identified from a random 20mer library panned against IR (SEQ ID NO:713).

Figure 2B: Formula 4 motif peptide sequences identified from a library constructed to contain variations in the F8 peptide (SEQ ID NO:713) as indicated (15% dope; referred to as "F815") panned against IR (SEQ ID NOS:714-796).

25 Figure 2C: Formula 4 motif peptide sequences identified from a library constructed to contain variations in the F8 peptide (SEQ ID NO:713) as indicated (15% dope; referred to as "F815") panned against IGF-1R (SEQ ID NOS:797-811).

Figure 2D: Formula 4 motif peptide sequences identified from a library constructed to contain variations in the F8 peptide (SEQ ID NO:

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713)as indicated (20% dope; referred to as "F820") panned against IR (SEQ ID NOS:812-861).

Figure 2E: Formula 4 motif peptide sequences identified from other libraries panned against IR (SEQ ID NOS:862-925).

5 Figure 3A: Formula 6 motif peptide sequences identified from a random 20mer library and panned against IR (SEQ ID NOS:926-928).

Figure 3B: Formula 6 motif peptide sequences identified from a library constructed to contain variations in the D8 peptide (SEQ ID NO: 929) as indicated (15% dope; referred to as "D815") panned against IR (SEQ ID
10 NOS:930-967).

Figure 3C: Formula 6 motif peptide sequences identified from a library constructed to contain variations in the D8 peptide (SEQ ID NO: 929) as indicated (20% dope; referred to as "D820") panned against IR (SEQ ID NOS:968-1010).

15 Figure 3D: Formula 6 motif peptide sequences identified from a library constructed to contain variations in the D8 peptide (SEQ ID NO: 929) as indicated (20% dope; referred to as "D820") panned against IGF-1R (SEQ ID NOS:1011-1059).

Figure 3E: Formula 6 motif peptide sequences identified from other
20 libraries panned against IR (SEQ ID NOS:1060-1061).

Figure 4A: Formula 10 motif peptide sequences identified from random 20mer libraries panned against IGF-1R (SEQ ID NOS:1062-1077).

Figure 4B: Formula 10 motif peptide sequences identified from random 20mer libraries panned against IR (SEQ ID NOS:1078-1082).

25 Figure 4C: Miscellaneous peptide sequences identified from a random 20mer library panned against IR (SEQ ID NOS:1083-1086).

Figure 4D: Miscellaneous peptide sequences identified from a random 40mer library panned against IR (SEQ ID NOS:1087-1088).

Figure 4E: Miscellaneous peptide sequences identified from a
30 random 20mer library panned against IGF-1R (SEQ ID NOS:1089-1092).

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Figure 4F: Miscellaneous peptide sequences identified from an X₁₋₄C X₆₋₂₀ library and panned against IGF-1R (SEQ ID NOS:1093-1113).

Figure 4G: Miscellaneous peptide sequences identified from a library constructed to contain variations of the F8 peptide(SEQ ID NO: 1114)
5 as indicated (F815) panned against IGF-1R (SEQ ID NOS:1115-1118).

Figure 4H: Miscellaneous peptide sequences identified from a library constructed to contain variations in the F8A11 peptide(SEQ ID NO: 1119) as indicated (referred to as "NNKH") panned against IR (SEQ ID NOS:1120-1142).

10 Figure 4I: Miscellaneous peptide sequences identified from a library constructed to contain variations in the F8A11 peptide(SEQ ID NO: 1119) as indicated (referred to as "NNKH") panned against IGF-1R (SEQ ID NOS:1143-1154).

Figure 5A: Summary of specific representative amino acid
15 sequences from Formulas 1, 4, 6, and 10 (SEQ ID NOS:1155-1180).

Figure 5B: Summary of specific representative amino acid sequences from Formulas 1, 4, 6, and 10 (SEQ ID NOS:1181-1220).

Figure 6: Illustration of 2 binding site domains on IR based on competition data.

20 Figure 7: Schematic illustration of potential binding schemes to the multiple binding sites on IR.

Figure 8: Biopanning results and sequence alignments of Group 1 of IR-binding peptides (SEQ ID NOS:1221-1243). The number of sequences found is indicated on the right side of the figure together with data on the phage binding to either IR or IGF-1R receptor. Absorbance
25 signals are indicated by: +++, >30X over background; ++, 15-30X; +, 5-15X; +, 2-5X; and 0, <2X.

Figures 9A-9B: Biopanning results and sequence alignments of Groups 2, 6, and 7 of IR-binding peptides (SEQ ID NOS:1244-1261). The
30 number of sequences found is indicated on the right side of the figure together with data on the phage binding to either IR or IGF-1R receptor.

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Absorbance signals are indicated by: +++, >30X over background; ++, 15-30X; +, 5-15X; 0, <2X.

Figures 10A-10C: Insulin competition data determined for various monomer and dimer peptides. Figure 10A shows the competition curve.
5 Figure 10B shows the symbol key for the peptides. Figure 10C shows the description of the peptides.

Figures 11A-11D: Insulin competition data determined for various monomer and dimer peptides. Figure 11A shows the competition curve. Figure 11B shows the symbol key for the peptides. Figure 11C shows the
10 description of the peptides. Figure 11D shows IR binding affinity for the peptides.

Figures 12A-12D: Results of free fat cell assays for truncated synthetic RP9 monomer peptides, S390 and S394. Figure 12A shows the results for peptide S390. Figure 12B shows the results for peptide S394.
15 Figure 12C shows the amino acid sequence of peptides S390 and S394 (SEQ ID NOS:1794 and 1788, respectively in order of appearance). Figure 12D shows the results for full-length RP9 peptide.

Figures 13A-13C: Results of free fat cell assays for truncated synthetic RP9 dimer peptides, S415 and S417. Figure 13A shows the
20 results for peptide S415. Figure 13B shows the results for peptide S417. Figure 13C shows the amino acid sequence of peptides S415 and S417 (SEQ ID NOS:1795-1796).

Figures 14A-14C: Results of free fat cell assays for RP9 homodimer peptides, 521 and 535. Figure 14A shows the results for
25 peptide 521. Figure 14B shows the results for peptide 535. Figure 14C shows the amino acid sequence of peptides 521 and 535.

Figures 15A-15C: Results of free fat cell assays for RP9-D8 heterodimer peptides, 537 and 538. Figure 15A shows the results for
30 peptide 537. Figure 15B shows the results for peptide 538. Figure 15C shows the amino acid sequence of peptides 537 and 538.

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Figures 16A-16C: Results of free fat cell assays for RP9-D8 heterodimer peptides 537 and 538. Figure 16A shows the results for peptide 537. Figure 16B shows the results for peptide 538. Figure 16C shows the amino acid sequence of peptides 537 and 538.

5 Figures 17A-17B: Results of free fat cell assays for D8-RP9 heterodimer peptide, 539. Figure 17A shows the results for peptide 539. Figure 17B shows the amino acid sequence of peptide 539.

Figures 18A-18D: Results of free fat cell assays for Site 1/Site 2 dimer peptides with constituent monomer peptides with Site 1-Site 2 C-N (Figure 18A), Site 1-Site 2, N-N (Figure 18B), Site 1-Site 2, C-C (Figure 18C), and Site 2-Site 1, C-N (Figure 18D) orientations and linkages, respectively.

Figures 19A-19B: Results of human insulin receptor kinase assays for various monomer and dimer peptides. Figure 19A shows the substrate phosphorylation curve. Figure 19B shows the EC₅₀ values.

Figures 20A-20B: Results of human insulin receptor kinase assays for Site 1-Site 2 and Site 2-Site 1 dimer peptides. Figure 20A shows the substrate phosphorylation curve. Figure 20B shows the EC₅₀ values.

Figures 21A-21B: Results of human insulin receptor kinase assays for Site 1-Site 2 and Site 2-Site 1 peptides. Figure 21A shows the substrate phosphorylation curve. Figure 21B shows the EC₅₀ values.

Figures 22A-22B: Results of time-resolved fluorescence resonance transfer assays for assessing the ability of various monomer and dimer peptides to compete with biotinylated RP9 monomer peptide for binding to soluble human insulin receptor-immunoglobulin heavy chain chimera. Figure 22A shows the binding curve. Figure 22B shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560, and 2001-2002, respectively in order of appearance).

Figures 23A-23C: Results of time-resolved fluorescence resonance transfer assays indicating the ability of various monomer and dimer peptide

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to compete with biotinylated S175 monomer peptide or biotinylated RP9 monomer peptide for binding to soluble human insulin receptor-immunoglobulin heavy chain chimera. Figures 23A-23B show the binding curves. Figure 23C shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560, and 2001-2002, respectively in order of appearance).

Figures 24A-24B: Results of fluorescence polarization assays indicating the ability of various monomer and dimer peptide to compete with fluorescein labeled RP9 monomer peptide for binding to soluble human insulin receptor ectodomain. Figure 24A shows the binding curve. Figure 24B shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560 and 2001-2002, respectively in order of appearance).

Figures 25A-25B: Results of fluorescence polarization assays indicating the ability of various monomer and dimer peptides to compete with fluorescein labeled RP9 monomer peptide for binding to soluble human insulin mini-receptor. Figure 25A shows the binding curve. Figure 25B shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560, and 2001-2002, respectively in order of appearance).

Figures 26A-26B: Results of fluorescence polarization assays indicating the ability of various monomer and dimer peptides to compete with fluorescein labeled insulin for binding to soluble human insulin receptor ectodomain. Figure 26A shows the binding curve. Figure 26B shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560, and 2001-2002, respectively in order of appearance).

Figures 27A-27B: Results of fluorescence polarization assays indicating the ability of various monomer and dimer peptides to compete with fluorescein labeled insulin for binding to soluble human insulin mini-

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receptor. Figure 27A shows the binding curve. Figure 27B shows the symbol key and description of the peptide sequences (SEQ ID NOS:2117, 1916-1917, 1558, 1994, 1960-1961, 2008, 1794, 2015-2016, 1560, and 2001-2002, respectively in order of appearance).

5 Figure 28: A schematic drawing for the construction of protein fusions of the maltose binding protein.

 Figure 29: BIAcore analysis of competition binding between IR and maltose binding protein fusion peptides H2C-9aa-H2C, H2C, and H2C-3aa-H2C.

10 Figure 30: Stimulation of IR autophosphorylation in vivo by maltose binding protein fusion peptides.

 Figures 31A-31C: Results of free fat cell assays for insulin and Site 2-Site 1 peptides, S519 and S520. Figure 31A shows the results for S519. Figure 31B shows the results for S520. Figure 31C shows the EC₅₀ values.

15 Figures 32A-32B: Results of human insulin receptor kinase assays for insulin and Site 2-Site 1 peptides S519 and S520. Figure 32A shows the substrate phosphorylation curve. Figure 32B shows the calculated Bestfit values.

 Figure 33: Results of *in vivo* experiments showing the effect of
20 intravenous administration of Site 2-Site 1 peptide S519 in Wistar rats:

 Figures 34A-34E: Results of phage competition studies with IGF-1 surrogates RP9 (Site 1) and D815 (Site 2) peptides. Phage: RP9 (A6-like); RP6 (B6-like); D8B12 (Site 2); and D815 (Site 2); Peptides: RP9 and D815. Figures 34A-34B show the competition curves. Figures 34C-34E show the
25 symbol keys and peptide groups.

 Figure 35A-35E: Phage competition studies with Site 2-Site 1 dimer peptides containing 6- or 12-amino acid linkers. Phage: RP9, RP6, D8B12, and D815; Peptides: D815-6L-RP9 and D815-12L-RP9. Figures 35A-35B show the competition curves. Figures 35C-35E show the symbol
30 keys and peptide groups.

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Figure 36: Results of IGF-1 agonist assay using FDCP-2 cells. Site 1 peptides RP6, RP9, G33, and Site 2 peptide D815 were tested in the agonist assay.

Figure 37: Results of IGF-1 antagonist assay using FDCP-2 cells.
5 Site 1 peptides RP6, RP9, G33, and Site 2 peptide D815 were tested in the antagonist assay.

Figure 38: Results of IGF-1 agonist assay using FDCP-2 cells. Site 1 peptides 20E2, S175, and RP9 were tested in the agonist assay.

Figures 39: Results of agonist and antagonist studies with surrogate
10 monomers and dimers. Monomers: D815 and RP9; Dimers: D815-6aa-RP9 and D815-12aa-RP9.

Figure 40: Results of agonist and antagonist studies with surrogate monomers and dimers. Monomers: G33 and D815; Dimer: D815-6aa-G33.

Figure 41: Results of agonist and antagonist studies with surrogate
15 peptides and dimers. Monomers: G33, D815 and RP9; Dimers: D815-6aa-RP9 and D815-12aa-RP9.

Figure 42: IGF-1 standard curve using FDCP-2 cells.

Figures 43A-43B: Peptide monomers identified from G33 and RP6 secondary libraries panned against IGF-1R (SEQ ID NOS:1262-1432).
20 Figure 43A shows peptides from G33 secondary library; Figure 43B shows peptides from RP6 secondary library.

Figures 44A-44B: Peptide dimers identified from libraries panned against IR or IGF-1R (SEQ ID NOS:1433-1540). Figure 44A shows dimer peptides panned against IR; Figure 44B shows dimer peptides panned
25 against IGF-1R.

Figure 45: Results of heterogeneous time-resolved fluorometric assays showing the effect of recombinant peptide surrogate G33 (rG33) on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

30 Figure 46: Results of heterogeneous time-resolved fluorometric assays showing the effect of recombinant peptide surrogate D815 (rD815)

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on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 47: Results of heterogeneous time-resolved fluorometric assays showing the effect of recombinant peptide surrogate RP9 on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 48: Results of heterogeneous time-resolved fluorometric assay showing the effect of recombinant peptide surrogate D815-6-G33 on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 49: Results of heterogeneous time-resolved fluorometric assays showing the effect of recombinant peptide surrogate D815-6-RP9 on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 50: Results of heterogeneous time-resolved fluorometric assays showing the effect of recombinant peptide surrogate D815-12-RP9 on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 51: Results of heterogeneous time-resolved fluorometric assays showing the effect of IGF-1 on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant human IGF-1R (rhIGF-1R).

Figure 52: Results of time-resolved fluorescence resonance energy transfer assays showing the effect of Site 1 peptide surrogates, Site 2 peptide surrogates, and rhIGF-1 on the dissociation of biotinylated-20E2 (b-20E2, Site 1) from recombinant human IGF-1R.

Figure 53: Results of time-resolved fluorescence resonance energy transfer assays showing the effect of various peptide monomers and dimers on the dissociation of biotinylated-20E2 (b-20E2, Site 1) from recombinant human IGF-1R.

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Figure 54: Results of glucose uptake assays in SGBS cells showing the potency of peptide S597 relative to human insulin.

Figure 55: Results of glucose-lowering assays in rats showing the potency of peptide S557 and S597 relative to human insulin.

5 Figure 56: Results of glucose-lowering assays in fasted Goettingen minipigs showing the potency of peptide S597 relative to human insulin.

Figure 57: Results of studies of disappearance of I¹²⁵-labelled peptides from site of injection.

V. DETAILED DESCRIPTION OF THE INVENTION

10 This invention relates to amino acid sequences comprising motifs that bind to the insulin receptor (IR) and/or insulin-like growth factor receptor (IGF-1R). In addition to binding to IR and/or IGF-1R, the amino acid sequences also possess either agonist, partial agonist or antagonist activity at IR or IGF-1R. In addition, the amino acid sequences bind to separate
15 binding sites (Sites 1 or 2) on IR or IGF-1R.

Although capable of binding to IR or IGF-1R at sites which participate in conferring agonist or antagonist activity, the amino acid sequences are not based on the native insulin or IGF-1 sequences, nor do they reflect an obvious homology to any such sequences.

20 The amino acid sequences of the invention may be peptides, polypeptides, or proteins. These terms as used herein should not be considered limiting with respect to the size of the various amino acid sequences referred to herein and which are encompassed within this invention. Thus, any amino acid sequence comprising at least one of the IR
25 or IGF-1R binding motifs disclosed herein, and which binds to IR or IGF-1R is within the scope of this invention. In preferred embodiments, the amino acid sequences confer insulin or IGF-1 agonist or antagonist activity. The amino acid sequences of the invention are typically artificial, i.e., non-naturally occurring, peptides, or polypeptides. Amino acid sequences useful
30 in the invention may be obtained through various means such as chemical

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synthesis, phage display, cleavage of proteins or polypeptides into fragments, or by any means which amino acid sequences of sufficient length to possess binding ability may be made or obtained.

5 The amino acid sequences provided by this invention should have an affinity for IR sufficient to provide adequate binding for the intended purpose. Thus, for use as a therapeutic, the peptide, polypeptide, or protein provided by this invention should have an affinity (K_d) of between about 10^{-7} to about 10^{-15} M. More preferably the affinity is 10^{-8} to about 10^{-12} M. Most preferably, the affinity is 10^{-10} to about 10^{-12} M. For use as a reagent in a competitive binding assay to identify other ligands, the amino acid sequence
10 preferably has affinity for the receptor of between about 10^{-5} to about 10^{-12} M.

The present invention describes several different binding motifs, which bind to active sites on IR or IGF-1R. The binding motifs are defined
15 based on the analysis of several different amino acid sequences and analyzing the frequency that particular amino acids or types of amino acids occur at a particular position of the amino acid sequence as described in the related applications of Beasley *et al.* International Application PCT/US00/08528, filed March 29, 2000, and Beasley *et al.*, U.S. Application
20 Serial No. 09/538,038, filed March 29, 2000.

Also included within the scope of this invention are amino acid sequences containing substitutions, additions, or deletions based on the teachings disclosed herein and which bind to IR or IGF-1R with the same or altered affinity. For example, sequence tags (e.g., FLAG® tags) or amino
25 acids, such as one or more lysines, can be added to the peptide sequences of the invention (e.g., at the N-terminal or C-terminal ends) as described in detail herein. Sequence tags can be used for peptide purification or localization. Lysines can be used to increase peptide solubility or to allow for biotinylation. Alternatively, amino acid residues located at the carboxy
30 and amino terminal regions of the consensus motifs described below, which comprise sequence tags (e.g., FLAG® tags), or which contain amino acid

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residues that are not associated with a strong preference for a particular amino acid, may optionally be deleted providing for truncated sequences. Certain amino acids (e.g., C-terminal or N-terminal residues) such as lysine which promote the stability or biotinylation of the amino acids sequences
5 may be deleted depending on the use of the sequence, as for example, expression of the sequence as part of a larger sequence which is soluble, or linked to a solid support.

Peptides that bind to IR or IGF-1R, and methods and kits for identifying such peptides, have been disclosed by Beasley *et al.*,
10 International Application PCT/US00/08528 filed March 29, 2000 and Beasley *et al.*, U.S. Application Serial No. 09/538,038 filed March 29, 2000, which are incorporated by reference in their entirety.

A. Consensus Motifs

The following motifs have been identified as conferring binding
15 activity to IR and/or IGF-1R:

1. $X_1X_2X_3X_4X_5$ (Formula 1; Group 1; the A6 motif) wherein X_1 , X_2 , X_4 and X_5 are aromatic amino acids, preferably, phenylalanine or tyrosine. Most preferably, X_1 and X_5 are phenylalanine and X_2 is tyrosine. X_3 may be any small polar amino acid, but is preferably selected from aspartic acid,
20 glutamic acid, glycine, or serine, and is most preferably aspartic acid or glutamic acid. X_4 is most preferably tryptophan, tyrosine, or phenylalanine and most preferably tryptophan. Particularly preferred embodiments of the A6 motif are FYDWF (SEQ ID NO:1554) and FYEWF (SEQ ID NO:1555). The A6 motif possesses agonist activity at IGF-1R, but agonist or antagonist
25 activity at IR depending on the identity of amino acids flanking A6. See Figure 5A.

Amino acid sequences that comprise the A6 motif and possess agonist activity at IR, include but are not limited to, D117/H2C: FHENFYDWFVRQVSKK (SEQ ID NO:1556); D117/H2 minus terminal
30 lysines: FHENFYDWFVRQVS (SEQ ID NO:1557); RP9:

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GSLDESFYDWFERQLGKK (SEQ ID NO:1558); RP9 minus terminal lysines: GSLDESFYDWFERQLG (SEQ ID NO:1559); and S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560). Preferred RP9 sequences include GLADEDIFYEWFERQLR (SEQ ID NO:1561),
 5 GLADEIFYEWFDRQLS (SEQ ID NO:1562), GQLDEDFYEWFDRLS (SEQ ID NO:1563), GQLDEDFYAWFDRLS (SEQ ID NO:1564), GFMDSEFYEWFERQLR (SEQ ID NO:1565), GFWDESFYAWFERQLR (SEQ ID NO:1566), GFMDSEFYAWFERQLR (SEQ ID NO:1567), and GFWDESFYEWFERQLR (SEQ ID NO:1568). Nonlimiting examples of
 10 Group 1 (Formula 1; A6) amino acid sequences are shown in Figures 1A-1O.

2. $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$ (Formula 2, Group 3; the B6 motif) wherein X_6 and X_7 are aromatic amino acids, preferably, phenylalanine or tyrosine. Most preferably, X_6 is phenylalanine and X_7 is tyrosine. X_8 , X_9 , X_{11} ,
 15 and X_{12} may be any amino acid. X_{10} and X_{13} are hydrophobic amino acids, preferably leucine, isoleucine, phenylalanine, tryptophan or methionine, but more preferably leucine or isoleucine. X_{10} is most preferably isoleucine for binding to IR and leucine for binding to IGF-1R. X_{13} is most preferably leucine. Amino acid sequences of Formula 2 may function as an antagonist
 20 at the IGF-1R, or as an agonist at the IR. Preferred consensus sequences of the Formula 2 motif are FYX₈X₉LX₁₁X₁₂L (SEQ ID NO:1569), FYX₈X₉IX₁₁X₁₂L (SEQ ID NO:1570), FYX₈ALX₁₁X₁₂L (SEQ ID NO:1571), and FYX₈YFX₁₁X₁₂L (SEQ ID NO:1572).

Another Formula 2 motif for use with this invention comprises FYX₈
 25 YFX₁₁X₁₂L (SEQ ID NO:1573) and is shown as Formula 2A ("NNRP") below: X₁₁₅X₁₁₆X₁₁₇X₁₁₈FYX₈YFX₁₁X₁₂LX₁₁₉X₁₂₀X₁₂₁X₁₂₂, (SEQ ID NO:1574) wherein X₁₁₅-X₁₁₈ and X₁₁₈-X₁₂₂ may be any amino acid which allows for binding to IR or IGF-1R. X₁₁₅ is preferably selected from the group consisting of tryptophan, glycine, aspartic acid, glutamic acid, and arginine.
 30 Aspartic acid, glutamic acid, glycine, and arginine are more preferred. Tryptophan is most preferred. The preference for tryptophan is based on its

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presence in clones at a frequency three to five fold higher than that expected over chance for a random substitution, whereas aspartic acid, glutamic acid and arginine are present about two fold over the frequency expected for random substitution.

- 5 X₁₁₆ preferably is an amino acid selected from the group consisting of aspartic acid, histidine, glycine, and asparagine. X₁₁₇ and X₁₁₈ are preferably glycine, aspartic acid, glutamic acid, asparagine, or alanine. More preferably X₁₁₇ is glycine, aspartic acid, glutamic acid and asparagine whereas X₁₁₈ is more preferably glycine, aspartic acid, glutamic acid or
- 10 alanine. X₈ when present in the Formula 2A motif is preferably arginine, glycine, glutamic acid, or serine. X₁₁ when present in the Formula 2A motif is preferably glutamic acid, asparagine, glutamine, or tryptophan, but most preferably glutamic acid. X₁₂ when present in the Formula 2A motif is preferably aspartic acid, glutamic acid, glycine, lysine or glutamine, but most
- 15 preferably aspartic acid. X₁₁₉ is preferably glutamic acid, glycine, glutamine, aspartic acid or alanine, but most preferably glutamic acid. X₁₂₀ is preferably glutamic acid, aspartic acid, glycine or glutamine, but most preferably glutamic acid. X₁₂₁ is preferably tryptophan, tyrosine, glutamic acid, phenylalanine, histidine, or aspartic acid, but most preferably tryptophan or
- 20 tyrosine. X₁₂₂ is preferably glutamic acid, aspartic acid or glycine; but most preferably glutamic acid. Preferred amino acid residue are identified based on their frequency in clones over two fold over that expected for a random event, whereas the more preferred sequences occur about 3-5 times as frequently as expected.
- 25 3. X₁₄X₁₅X₁₆X₁₇X₁₈X₁₉X₂₀X₂₁ (Formula 3, reverse B6, revB6), wherein X₁₄ and X₁₇ are hydrophobic amino acids; X₁₄, X₁₇ are preferably leucine, isoleucine, and valine, but most preferably leucine; X₁₅, X₁₆, X₁₈ and X₁₉ may be any amino acid; X₂₀ is an aromatic amino acid, preferably tyrosine or histidine, but most preferably tyrosine; and X₂₁ is an aromatic
- 30 amino acid, but preferably phenylalanine or tyrosine, and most preferably

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phenylalanine. For use as an IGF-1R binding ligand, an aromatic amino acid is strongly preferred at X₁₈.

4. X₂₂X₂₃X₂₄X₂₅X₂₆X₂₇X₂₈X₂₉X₃₀X₃₁X₃₂X₃₃X₃₄X₃₅X₃₆X₃₇X₃₈X₃₉X₄₀
X₄₁ (Formula 4; Group 7; the F8 motif) wherein X₂₂, X₂₅, X₂₆, X₂₈, X₂₉, X₃₀,
5 X₃₃, X₃₄, X₃₅, X₃₆, X₃₇, X₃₈, X₄₀, and X₄₁ are any amino acid. X₃₅ and X₃₇ may
be any amino acid when the F8 motif is used as an IR binding ligand or as a
component of an IR binding ligand, however for use as an IGF-1R binding
ligand, glycine is strongly preferred at X₃₇ and a hydrophobic amino acid,
particularly, leucine, is preferred at X₃₅. X₂₃ is a hydrophobic amino acid.
10 Methionine, valine, leucine or isoleucine are preferred amino acids for X₂₃,
however, leucine which is most preferred for preparation of an IGF-1R
binding ligand is especially preferred for preparation of an IR binding ligand.
At least one cysteine is located at X₂₄ through X₂₇, and one at X₃₉ or X₄₀.
Together the cysteines are capable of forming a cysteine cross-link to create
15 a looped amino acid sequence. In addition, although a spacing of 14 amino
acids in between the two cysteine residues is preferred, other spacings may
also be used provided binding to IGF-1R or IR is maintained. Accordingly,
other amino acids may be substituted for the cysteines at positions X₂₄ and
X₃₉ if the cysteines occupy other positions.
20 In one embodiment, for example, the cysteine at position X₂₄ may
occur at position X₂₇ which will produce a smaller loop provided that the
cysteine is maintained at position X₃₉. These smaller looped peptides are
described herein as Formula 5, infra. X₂₇ is any polar amino acid, but is
preferably selected from glutamic acid, glutamine, aspartic acid, asparagine,
25 or as discussed above cysteine. The presence of glutamic acid at position
X₂₇ decreases binding to IR but has less of an effect on binding to IGF-1R.
X₃₁ is any aromatic amino acid and X₃₂ is any small amino acid. For binding
to IGF-1R, glycine or serine is preferred at position X₃₁, however, tryptophan
is highly preferred for binding to IR. At position X₃₂, glycine is preferred for
30 both IGF-1R and IR binding. X₃₆ is an aromatic amino acid. A preferred
consensus sequence for F8 is X₂₂ LC X₂₅ X₂₆ E X₂₈ X₂₉ X₃₀ WG X₃₃ X₃₄ X₃₅

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X₃₆ X₃₇ X₃₈ C X₄₀ X₄₁ (SEQ ID NO:1575) whereas the amino acids are defined above. A more preferred F8 sequence is HLCVLEELFWGASLFGYCSG ("F8"; SEQ ID NO:1576). Amino acid sequences comprising the F8 sequence motif preferably bind to IR over
 5 IGF-1R. Figures 2A-2E list nonlimiting examples of Formula 4 amino acid sequences.

5. X₄₂ X₄₃ X₄₄ X₄₅ X₄₆ X₄₇ X₄₈ X₄₉ X₅₀ X₅₁ X₅₂ X₅₃ X₅₄ X₅₅ X₅₆ X₅₇ X₅₈ X₅₉ X₆₀ X₆₁ (Formula 5; mini F8 motif) wherein X₄₂, X₄₃, X₄₄, X₄₅, X₅₃, X₅₅, X₅₆, X₅₈, X₆₀ and X₆₁ are any amino acid. X₄₃, X₄₆, X₄₉, X₅₀ and X₅₄ are
 10 hydrophobic amino acids, however, X₄₃ and X₄₆ are preferably leucine, whereas X₅₀ is preferably phenylalanine or tyrosine but most preferably phenylalanine. X₄₇ and X₅₉ are cysteines. X₄₈ is preferably a polar amino acid, i.e., aspartic acid or glutamic acid, but most preferably glutamic acid. Use of the small amino acid at position 54 may confer IGF-1R specificity.
 15 X₅₁, X₅₂, and X₅₇ are small amino acids, preferably glycine. A preferred consensus sequence for mini F8 is X₄₂ X₄₃ X₄₄ X₄₅ L C E X₄₉ F G G X₅₃ X₅₄ X₅₅ X₅₆ G X₅₈ C X₆₀ X₆₁ (SEQ ID NO:1577). Amino acid sequences comprising the sequence of Formula 5 preferably bind to IGF-1R or IR.

6. X₆₂ X₆₃ X₆₄ X₆₅ X₆₆ X₆₇ X₆₈ X₆₉ X₇₀ X₇₁ X₇₂ X₇₃ X₇₄ X₇₅ X₇₆ X₇₇ X₇₈ X₇₉ X₈₀ X₈₁ (Formula 6; Group 2; the D8 motif) wherein X₆₂, X₆₅, X₆₈, X₆₉, X₇₁, X₇₃, X₇₆, X₇₇, X₇₈, X₈₀ and X₈₁ may be any amino acid. X₆₆ may also be any amino acid, however, there is a strong preference for glutamic acid. Substitution of X₆₆ with glutamine or valine may result in attenuation of binding. X₆₃, X₇₀, and X₇₄ are hydrophobic amino acids. X₆₃ is preferably
 25 leucine, isoleucine, methionine, or valine, but most preferably leucine. X₇₀ and X₇₄ are preferably valine, isoleucine, leucine, or methionine. X₇₄ is most preferably valine. X₆₄ is a polar amino acid, more preferably aspartic acid or glutamic acid, and most preferably glutamic acid. X₆₇ and X₇₅ are aromatic amino acids. Whereas tryptophan is highly preferred at X₆₇, X₇₅ is preferably
 30 tyrosine or tryptophan but most preferably tyrosine. X₇₂ and X₇₉ are

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cysteines that again are believed to form a loop which position amino acid may be altered by shifting the cysteines in the amino acid sequence.

D8 is most useful as an amino acid sequence having a preference for binding to IR as only a few D8 sequences capable of binding to IGF-1R over background have been detected. A preferred sequence for binding to IR is
 5 X₆₂ L X₆₄ X₆₅ X₆₆ W X₆₈ X₆₉ X₇₀ X₇₁ C X₇₃ X₇₄ X₇₅ X₇₆ X₇₇ X₇₈ C X₈₀ X₈₁ (SEQ ID NO:1578). Examples of specific peptide sequences comprising this motif include D8: KWLDQEWAWVQCEVYGRGCPSKK (SEQ ID NO:1579); and D8 minus terminal lysines: KWLDQEWAWVQCEVYGRGCPS (SEQ ID
 10 NO:1580). Preferred D8 monomer sequences include SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581) and SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582). Preferred D8 dimer sequences include SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583), and SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584). Nonlimiting examples
 15 of Group 2 (Formula 6; D8) amino acid sequences are shown in Figures 3A-3E.

7. H X₈₂, X₈₃, X₈₄ X₈₅ X₈₆ X₈₇ X₈₈ X₈₉ X₉₀ X₉₁ X₉₂ (Formula 7) wherein X₈₂ is proline or alanine but most preferably proline; X₈₃ is a small amino acid more preferably proline, serine or threonine and most preferably
 20 proline; X₈₄ is selected from leucine, serine or threonine but most preferably leucine; X₈₅ is a polar amino acid preferably glutamic acid, serine, lysine or asparagine but more preferably serine; X₈₆ may be any amino acid but is preferably a polar amino acid such as histidine, glutamic acid, aspartic acid, or glutamine; X₈₇ is an aliphatic amino acid preferably leucine, methionine or
 25 isoleucine and most preferably leucine; amino acid X₈₈, X₈₉ and X₉₀ may be any amino acids; X₉₁ is an aliphatic amino acid with a strong preference for leucine as is X₉₂. Phenylalanine may also be used at position 92. A preferred consensus sequence of Formula 7 is H P P L S X₈₆ L X₈₈ X₈₉ X₉₀ L L (SEQ ID NO:1585). The Formula 7 motif binds to IR with little or no
 30 binding to IGF-1R.

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8. Another sequence is $X_{104} X_{105} X_{106} X_{107} X_{108} X_{109} X_{110} X_{111} X_{112} X_{113} X_{114}$ (Formula 8) which comprises eleven amino acids wherein at least one, and preferably two of the amino acids of X_{106} through X_{111} are tryptophan. In addition, it is also preferred that when two tryptophan amino acids are present in the sequence they are separated by three amino acids, which are preferably, in sequential order proline, threonine and tyrosine with proline being adjacent to the tryptophan at the amino terminal end. Accordingly, the most preferred sequence for $X_{107} X_{108} X_{109} X_{110} X_{111}$ is WPTYW (SEQ ID NO:1586). At least one of the three amino acids on the amino terminal ($X_{104}, X_{105} X_{106}$) and at least one of the amino acids carboxy terminal ($X_{112} X_{113} X_{114}$) ends immediately flanking X_{107} - X_{111} are preferably a cysteine residue, most preferably at X_{105} and X_{113} respectively. Without being bound by theory, the cysteines are preferably spaced so as to allow for the formation of a loop structure. X_{104} and X_{114} are both small amino acids such as, for example, alanine and glycine. Most preferably, X_{104} is alanine and X_{114} is glycine. X_{105} may be any amino acid but is preferably valine. X_{112} is preferably asparagine. Thus, the most preferred sequence is ACVWPTYWNCG (SEQ ID NO:1587).

9. An amino acid sequence comprising JBA5: DYKDLQCQSWGVRIGWLAGLCPKK (SEQ ID NO:1541); or JBA5 without terminal lysines: LCQSWGVRIGWLAGLCP (SEQ ID NO:1542) (Formula 9). The Formula 9 motif is another motif believed to form a cysteine loop that possesses agonist activity at both IR and IGF-1R. Although IR binding is not detectable by ELISA, binding of Formula 9 to IR is competed by insulin and is agonistic.

10. $W X_{123} G Y X_{124} W X_{125} X_{126}$ (SEQ ID NO:1543) (Formula 10; Group 6) wherein X_{123} is selected from proline, glycine, serine, arginine, alanine or leucine, but more preferably proline; X_{124} is any amino acid, but preferably a charged or aromatic amino acid; X_{125} is a hydrophobic amino acid preferably leucine or phenylalanine, and most preferably leucine. X_{126} is any amino acid, but preferably a small amino acid. In one embodiment of

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the present invention, the Formula 10, Group 6 motif is WPGY (SEQ ID NO: 1588). Examples of specific peptide sequences comprising this motif include E8: KVRGFQGGTVWPGYEWLRNAKK (SEQ ID NO:1589); and E8 minus terminal lysines: KVRGFQGGTVWPGYEWLRNAA (SEQ ID NO:1590). Preferred Group 6 sequences include WAGYEW (SEQ ID NO:1591), WEGYEWL (SEQ ID NO:1592), WAGYEWL (SEQ ID NO:1593), WEGYEW (SEQ ID NO:1594), and DSDWAGYEWFEQLD (SEQ ID NO:1595). Nonlimiting examples of Group 6 amino acid sequences are shown in Figures 4A-4B.

The IR and IGF-1R binding activities of representative Group 1 (Formula 1; A6); Group 2 (Formula 6; D8); and Group 6 (Formula 10); and Group 7 (Formula 4; F8) amino acid sequences are summarized in Figures 8 and 9A-9B. Group 1 (Formula 1; A6) amino acid sequences contain the consensus sequence FyxWF (SEQ ID NO:1596), which is typically agonistic in cell-based assays. Group 2 (Formula 6; D8) amino acid sequences are composed of two internal sequences having a consensus sequence VYGR (SEQ ID NO:1597) and two cysteine residues each. Thus, Group 2 peptides are capable of forming a cyclic peptide bridged with a disulfide bond. Neither of these consensus sequences have any significant linear sequence similarities greater than 2 or 3 amino acids with mature insulin. Group 7 (Formula 4; F8) amino acid sequences are composed of two internal exemplary sequences which do not have any significant sequence homology, but have two cysteine residues 13-14 residues apart, thus being capable of forming a cyclic peptide with a long loop anchored by a disulfide bridge.

B. Amino And Carboxyl Terminal Extensions Modulate Activity of Motifs

In addition to the motifs stated above, the invention also provides preferred sequences at the amino terminal or carboxyl terminal ends which are capable of enhancing binding of the motifs to either IR, IGF-1R, or both. In addition, the use of the extensions described below does not preclude the

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possible use of the motifs with other substitutions, additions or deletions that allow for binding to IR, IGF-1R, or both.

1. Formula 1

Any amino acid sequence may be used for extensions of the amino
5 terminal end of A6, although certain amino acids in amino terminal
extensions may be identified which modulate activity. Preferred carboxy
terminal extensions for A6 are A6 X₉₃ X₉₄ X₉₅ X₉₆ X₉₇ wherein X₉₃ may be
any amino acid, but is preferably selected from the group consisting of
alanine, valine, aspartic acid, glutamic acid, and arginine, and X₉₄ and X₉₇
10 are any amino acid; X₉₅ is preferably glutamine, glutamic acid, alanine or
lysine but most preferably glutamine. The presence of glutamic acid at X₉₅
however may confer some IR selectivity. Further, the failure to obtain
sequences having an asparagine or aspartic acid at position X₉₅ may
indicate that these amino acids should be avoided to maintain or enhance
15 sufficient binding to IR and IGF-1R. X₉₆ is preferably a hydrophobic or
aliphatic amino acid, more preferably leucine, isoleucine, valine, or
tryptophan but most preferably leucine. Hydrophobic residues, especially
tryptophan at X₉₆ may be used to enhance IR selectivity.

2. Formula 2

20 B6 with amino terminal and carboxy terminal extensions may be
represented as X₉₈ X₉₉ B6 X₁₀₀. X₉₈ is optionally aspartic acid and X₉₉ is
independently an amino acid selected from the group consisting of glycine,
glutamine, and proline. The presence of an aspartic acid at X₉₈ and a
proline at X₉₉ is associated with an enhancement of binding for both IR and
25 IGF-1R. A hydrophobic amino acid is preferred for the amino acid at X₁₀₀, an
aliphatic amino acid is more preferred. Most preferably leucine, for IR and
valine for IGF-1R. Negatively charged amino acids are preferred at both the
amino and carboxy terminals of Formula 2A.

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3. Formula 3

An amino terminal extension of Formula 3 defined as $X_{101} X_{102} X_{103}$ revB6 wherein X_{103} is a hydrophobic amino acid, preferably leucine, isoleucine or valine, and X_{102} and X_{101} are preferably polar amino acids, more preferably aspartic acid or glutamic acid may be useful for enhancing binding to IR and IGF-1R. No preference is apparent for the amino acids at the carboxy terminal end of Formula 3.

4. Formula 10

In one preferred embodiment, Formula 10 sequences $W X_{123} G Y X_{124} W X_{125} X_{126}$ (SEQ ID NO:1543) can include an amino terminal extension comprising the sequence DSD and/or a carboxy terminal extension comprising the sequence EQLD (SEQ ID NO:1598).

C. IR Binding Preferences

As indicated above, the amino acid sequences containing the motifs of this invention may be constructed to have enhanced selectivity for either IR or IGF-1R by choosing appropriate amino acids at specific positions of the motifs or the regions flanking them. By providing amino acid preferences for IR or IGF-1R, this invention provides the means for constructing amino acid sequences with minimized activity at the non-cognate receptor. For example, the amino acid sequences disclosed herein with high affinity and activity for IR and low affinity and activity for IGF-1R are desirable as IR agonist as their propensity to promote undesirable cell proliferation, an activity of IGF-1 agonists, is reduced. Ratios of IR binding affinity to IGF-1R binding affinity for specific sequences are provided in Figures 1A-1O; 2A-2E; 3A-3E; 4A-4I; 44A-44B. As an insulin therapeutic, the IR/IGF-1R binding affinity ratio is preferably greater than 100. Conversely, for use as an IGF-1R therapeutic, the IR/IGF-1R ratio should be less than 0.01. Examples of peptides that selectively bind to IGF-1R are shown below.

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TABLE 1

IGF-1R-SELECTIVE SEQUENCES

FORMULA 1 (Group 1; A6-like):

Ratios over Background Comparisons

Clone	SEQ ID NO:	Sequence	E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
A6L-0-E6-IR	1599	YRGMLVIGRSSDAGKVAERPARIGQTFVAVNFYDFV	31.0	31.0	1.8	17.0	0.1
H2CA-4-G9-IGFR	1600	GIISQCPESFYDWPAGQVSDPWNCW	8.6	9.5	0.6	16.0	0.1
H2CA-4-H6-IGFR	1601	VGRASGFENFYDWFGRQISLQGEQ	4.9	10.5	0.7	14.6	0.1
A6L-0-E4-IR	1602	YRGMLVIGRISDAG#VASEPPARIGRKVFAVNFYDFV	26.0	16.0	1.3	13.0	0.1
A6L-0-H3-IR	1603	YRGMLVIGRISGGAGAAASERPARIGQKVSANFYDFV	27.0	26.0	2.0	13.0	0.1
H2CA-4-F5-IGFR	1604	VGYQGQDENFYDWFIRQVSGRLGQ	5.5	9.7	0.8	12.3	0.1
H2CA-4-H8-IGFR	1605	SACQFDCHENFYDWFARQVSGGAAYG	5.6	9.2	1.0	9.4	0.1
H2CA-4-F11-IGFR	1606	SAAQLFFQESFYDWFPLRQVAESSQPN	3.5	6.8	1.0	6.7	0.1
H2CA-4-F6-IGFR	1607	AVRATRFDEAFYDWFVROI SDQGNK	3.9	7.3	1.1	6.4	0.2
H2CA-4-F10-IGFR	1608	VNQSISIENFYDWFEROVSHQGRV	4.9	5.7	1.0	5.9	0.2
H2CA-1-A3-IGFR	1609	APDPDFQEIFYDWFVRQVSRPFGG	7.7	3.8	0.8	5.1	0.2
H2CA-3-C8-IGFR	1610	SSCDGAGHSFYENFVRQVSGCRSV	15.1	5.6	1.2	4.8	0.2
H2CA-2-B9-IGFR	1611	RAGSDFHEDFYENFVRQVSLKKG	9.3	7.0	1.7	4.2	0.2
H2CA-4-H4-IGFR	1612	QAVQGFHEEFYDWFVRQVSTGVGG	3.9	4.1	1.0	4.2	0.2
E4Dq-4-H2-IR	1613	GFREGNFYENFQAQT	37.8	33.9	8.2	4.1	0.2
H2CA-4-F7-IGFR	1614	SSIGGFHENFYDWFNRQISQSPPLK	1.5	3.2	0.8	4.1	0.2
H2CA-3-D6-IGFR	1615	QSPVGSSEDFYDWFRRQVQAQGAHQ	8.3	9.0	2.2	4.0	0.3
H2CA-3-D8-IGFR	1616	NYRRQVFNGNFYDWFDRQVFSLVTPG	10.9	7.2	1.8	4.0	0.3
H2CA-4-G11-IGFR	1617	TLDGGSFEEQFYDWFVRQISYRTNPD	10.8	9.5	2.5	3.9	0.3
H2CA-4-F1-IGFR	1618	FVYQQGHENFYDWFDRQVQSQGGAG	5.8	3.5	0.9	3.8	0.3
H2CA-3-D7-IGFR	1619	LRRQAPVEENFYDWFVRQVSGRVGG	13.3	3.0	0.8	3.7	0.3
H2CA-1-A7-IGFR	1620	RCGRELYHSTFYDWFDRQVAGRTCPs	8.0	2.2	0.6	3.7	0.3
H2CA-2-B4-IGFR	1621	CCLLCRFQQNFYDWFVCOGISLRPL	3.5	4.1	1.1	3.6	0.3
H2CA-2-B3-IGFR	1622	PLASDLVDQFYGYHVFVQVSPPRGG	7.7	3.8	1.0	3.6	0.3
H2CA-2-B2-IGFR	1623	GAPVDQLHEDFYDWFVRQVQAATG	4.1	3.4	1.0	3.5	0.3
E4Dq-2-D11-IR	1624	GFREGSFYDWFQAQT	40.2	11.1	3.3	3.4	0.3
20E2Bβ-4-G6-IR	1625	SQAGSAFYANFDQVIRTVHSA	22.4	6.2	1.9	3.3	0.3
H2CA-4-H9-IGFR	1626	RCVAGFHDQFYDWFDRQVSRVHKFG	8.7	5.6	1.9	3.0	0.3

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Ratios over Background Comparisons

Clone	SEQ ID NO:	Sequence	E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
H2CA-2-B11-IGFR	1627	AICDAGFHEFYDFWALQVSDGCRQS	11.9	4.6	1.6	3.0	0.3
H2CA-3-E8-IGFR	1628	LGYPEPQQNFYDFVQVSGAENAG	13.2	6.3	2.2	2.9	0.3
A6S-2-D11-IR	1629	EAASLGSQDRNFYDFVFRQVV	48.4	37.4	13.5	2.8	0.4
A6S-2-D1-IR	1630	VERSASSQDNFYDFVQVQIR	37.8	30.6	12.0	2.6	0.4
A6S-3-E2-IR	1631	TSEVQRRSQDNFYDFVQAQA	33.1	24.7	9.8	2.5	0.4
H2CA-3-E11-IGFR	1632	HLADGFHEKXFYDFWFERQISSRNCDC	4.7	2.2	1.0	2.2	0.5
H2CA-3-C11-IGFR	1633	FRTLAQHDsfYDFWDRQVSGAGER	9.3	3.3	1.6	2.1	0.5
A6-PD1-IGFR	1634	SFHEDFYDFWDRQVSGSLKK					
H2C-PD1-IGFR (RP9)	1558	GSLDESFYDFWFERQLGKK					

FORMULA 2 (Group 2; B6-like):

Ratios over Background Comparisons

Clone	SEQ ID NO:	Sequence	E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
20C-3-G3-IGFR	1635	TFYSCIASLLTGTQPNRGPWERC	33.1	32.3	1.2	27.0	<0.1
20C-4-C7-IGFR	1636	PFYDCLAALQGVARYHDLCAVEIT	35.3	28.0	1.3	21.8	<0.1
B6Ha-1-B5-IR	1637	CCTTEVMVDARDPFFYHKLSELVTGG	41.5	20.5	1.0	20.5	0.0
R20β-4-A6-IR	1638	RQSDAFYSGIMALIGLSDG	9.3	25.9	1.5	17.3	0.1
20E2B-1-A6-IGFR	1639	GVRAMSFYDALVSVLGLPSG	18.6	18.1	1.1	16.8	0.1
R20α-4-20A12-IR	1640	RLFYCGIQALGANLGYSGCV	48.6	39.9	2.4	16.6	0.1
20E2Bβ-4-G7-IR	1641	LQPCSGFYECIERLIGVKLSG	19.9	25.2	1.6	15.8	0.1
NNRPγ-4-B11-IR	1642	LKDGFDYFWQRLHLS	4.1	18.7	1.2	15.5	0.1
20E2B-3-C6-IGFR	1643	VEGRGLFYDLLRQLLARRQNG	17.9	16.8	1.1	14.8	0.1
B6Ha-1-A2-IR	1644	RGCNDGKGWSDPFFYHKLSELICGG	22.3	14.6	1.0	14.6	0.1
20E2A-4-F11-IGFR	1645	QGGSAFYDAIDRLRMRIIG	21.3	18.8	1.3	14.6	0.1
B6Ha-3-E9-IR	1646	RCEKQAEVGFSSDFFYHKMSSELLGCR	44.6	24.2	1.7	14.2	0.1
20C-3-F6-IGFR	1647	DRDFCFYERLTLVGGQVDGWPCC	33.5	26.1	1.9	14.1	0.1
20E2B-4-H3-IGFR	1648	KLHNLFFYGLQRLVWAGLIG	11.2	14.8	1.1	13.9	0.1
20E2B-3-C2-IGFR	1649	GNGDGMFYQLLSLLVGRDMHV	13.1	8.9	0.6	13.8	0.1
20C-3-A1-IGFR	1650	SSYCGDGYLMLFSGLIVASQELC	26.5	20.8	1.5	13.7	0.1
20E2B-3-E3-IGFR	1651	PDHKGFYAQLAQLIRGQLLS	22.4	16.3	1.3	13.1	0.1
R20α-3-20E2-IR	1652	FYDAIDQLVRGSARAGGTRD	46.3	39.9	3.1	12.9	0.1
20E2B-4-H12-IGFR	1653	YSCGDGFYSLSDLLGGQFRC	6.5	9.7	0.8	12.8	0.1
B6Ha-3-F11-IR	1654	RGMKEEVLVGSTDPFFYHKLSELLQGS	49.5	18.7	1.6	11.7	0.1

Ratios over Background Comparisons

Clone	SEQ ID NO:	Sequence	E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
20E2B-3-D2-IGFR	1655	IQBELTFYDLLHRLVRSELGS	20.7	12.4	1.1	11.7	0.1
20E2B-3-D8-IGFR	1656	GGTEVDFTYRALERLVRGQLGL	20.4	17.7	1.6	11.3	0.1
20E2B-3-E8-IGFR	1657	LRIANLFYQRLWDLAFFGGG	15.7	16.7	1.5	11.1	0.1
B6Hα-2-C4-IR	1658	RCGRW*AEAGAGDDPFYHKLSELVCG	20.7	9.9	0.9	11.0	0.1
R20α-4-20C11-IR	1659	DRAFYNGRLDLVGAUVYGAWD	43.7	30.8	3.0	10.3	0.1
20E2B-4-F8-IGFR	1660	PVGQGFYEGLSRLVLGRGGW	12.3	7.3	0.8	9.7	0.1
20E2B-1-A11-IGFR	1661	RFSTDGFYQLLALVGGPVG	15.0	9.5	1.0	9.7	0.1
20E2B-3-D4-IGFR	1662	NSRDGGFYQLERLLGFPVVG	8.1	7.9	0.8	9.6	0.1
20E2B-2-B11-IGFR	1663	VVTPVNFYRALEALVRG.RLG	13.9	10.6	1.1	9.4	0.1
20E2B-3-C8-IGFR	1664	QAPDPGFYSALMKLIGRGVS	18.5	15.6	1.8	8.9	0.1
20E2B-2-B2-IGFR	1665	PGTDLGFYQALRCVVIQACD	11.7	4.9	0.6	8.1	0.1
20E2B-4-F10-IGFR	1666	AQPCGGFYGLLEQLVGRSVCD	19.0	17.3	2.2	7.8	0.1
20E2B-4-F9-IGFR	1667	QPDHSYFYSLLQELVGEERL	11.9	14.7	1.9	7.7	0.1
20C-3-A4-IGFR	1668	QFYGCLLDLSLGVPSFGWRRRCITTA	17.7	8.8	1.2	7.6	0.1
20E2B-3-D11-IGFR	1669	LGVTDFYAAALGYLIHVGQF	14.3	12.2	1.6	7.6	0.1
20E2B-3-C11-IGFR	1670	CMV.DGFYAGLGLLTAGEGR	15.3	15.4	2.1	7.5	0.1
20E2B-2-B3-IGFR	1671	ICTGQGFYQVLCGLLRGTSAR	9.1	5.3	0.7	7.4	0.1
20E2B-3-D12-IGFR	1672	QGNVLDIFYGWIGRLLAKQGS	10.3	6.2	0.9	7.3	0.1
20E2B-3-E12-IGFR	1673	VATSQGFYSGLSELQGGNV	13.9	6.0	0.8	7.3	0.1
20E2B-2-B8-IGFR	1674	IWATGDFYRLLSQLVMGRVGT	17.4	5.7	0.8	7.2	0.1
NNRPY-4-A9-IR	1675	EGSGFYGYFFSLGLQG	3.0	10.0	1.4	7.1	0.1
20E2B-4-G11-IGFR	1676	RQGTGSFYLMLEQLVVGARGP	8.9	4.5	0.6	7.0	0.1
20E2B-3-D6-IGFR	1677	DSVGDNFYQLLESVLGGHVG	20.7	17.8	2.6	6.9	0.1
B6Hα-2-C7-IR	1678	RGIVAMVEATEVSGDHPFYHKLSELVQGS	45.1	6.7	1.0	6.7	0.1
20E2B-2-B7-IGFR	1679	LSSDGFYRALNLLQGSAGR	18.0	6.1	0.9	6.7	0.1
20E2B-3-C4-IGFR	1680	ASSAGFYELLQRLAGIGLEV	23.4	20.4	3.3	6.2	0.2
20C-3-E4-IGFR	1681	FFYRCLSRLLGGQLGSRLLGSCIGD	37.7	7.7	1.3	6.0	0.2
NNRPY-4-A1-IR	1682	IIGGFYSYFNSVLRIGT	9.7	10.9	1.8	6.0	0.2
20E2B-4-H8-IGFR	1683	PAGCGFYCGIGLILHGDQSP	7.2	5.3	0.9	5.9	0.2
20E2B-4-H9-IGFR	1684	RCQGTGYTYCIQELIGFGDPD	4.5	5.2	0.9	5.6	0.2
B6Hα-2-C10-IR	1685	SGAKVIVTGDSDGDPFYHKLSELVQGS	46.9	5.8	1.1	5.3	0.2
20E2A-3-C7-IGFR	1686	VGTVAGFYDAIAQLVARASRV	17.6	5.4	1.1	5.1	0.2
20E2B-1-A8-IGFR	1687	TLRSPFTFYDWMLEWLVTHGQGG	16.1	4.4	0.9	5.0	0.2
NNRPY-4-A7-IR	1688	RFDPFYSYFVNLLGASA	2.5	6.3	1.3	4.9	0.2

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Ratios over Background Comparisons

Clone	SEQ ID NO:	Sequence	E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
B6Hα-3-E8-IR	1689	RGKTAIVIGRPADPFYHKLSELLQGG	47.6	5.3	1.1	4.8	0.2
B6Hα-3-F10-IR	1690	GCVEWQKHCASDPFYHKLSELGGCS	47.2	8.8	1.9	4.6	0.2
B6Hα-2-D6-IR	1691	GRTMAVAAAGPDDPFYHKLSELVQGG	33.5	4.4	1.0	4.4	0.2
B6Hα-3-E7-IR	1692	GCAVVERAERSRGGDPFYHKLSELLQGC	47.0	5.6	1.3	4.3	0.2
B6Hα-2-D1-IR	1693	GCEVIVEEGDSADPFYHKLSELQCGS	11.7	5.4	1.3	4.2	0.2
20E2A-3-D10-IGFR	1694	MMVVDGFYDALHQLVVAQSLG	20.6	6.9	1.8	3.9	0.3
20E2A-3-A12-IGFR	1695	LSVALSFYDALGQLVAGEGRW	16.1	4.3	1.1	3.9	0.3
B6Hα-4-G8-IR	1696	GGTKAVAKVGTDRDDPFYHKLSELLQGS	32.3	6.1	1.7	3.6	0.3
B6L-4-D7-IR	1697	AETSVQVGWIRLQSVMPGHEWNTVDPFYHKLSELLRGSGA	14.3	4.8	1.4	3.4	0.3
B6Hα-1-A3-IR	1698	SRKVEAEMPDSGDPFYHKLSELLASG	37.4	2.6	0.8	3.3	0.3
B6Hα-3-F7-IR	1699	SRVAATKEKRPSDDPFYHKLSELLQGS	41.5	3.1	1.0	3.1	0.3
B6Hα-2-D8-IR	1700	SSETAKWVTGTDRDDPFYHKLSELVQGS	19.3	3.0	1.0	3.0	0.3
B6Hα-1-B3-IR	1701	GCITAENGAGDPFYHKLSELGGCS	33.1	3.2	1.1	2.9	0.3
B6Hα-3-E5-IR	1702	RCGDEEGQENRRDDPFYHKLSELFGGC	28.8	2.9	1.0	2.9	0.3
20E2A-4-G11-IGFR	1703	MMVFSFYDAIDQLVCQRIGC	20.7	3.3	1.3	2.6	0.4
20E2Bβ-3-C7-IR	1704	QSGSGDFYDWLSRLIRNGDGG	1.5	3.1	1.5	2.0	0.5
B6Hα-3-E6-IR	1705	CGAKMTGTPNDPFYHKLSELLQRG	18.2	2.3	1.2	1.9	0.5
20E2A-3-A3-IGFR	1706	GHYFGSFYDAIDQLVAGMLPG	5.2	3.0	1.5	1.9	0.5
B6L-4-A7-IR	1707	AGTPAQVG*NRLMSVMPGHEWNTVDPFYHKLSELLRESGA	11.6	3.4	1.9	1.8	0.6
B6Hα-3-F1-IR	1708	CSMAVAEAGDDDDPFYHKLSELQCGS	22.5	2.4	1.3	1.8	0.5
B6L-3-G6-IR	1709	VDTPAQVGNRLMSVMPGHEWYTDPPFYH*LSELLRESGA	7.6	2.5	1.8	1.4	0.7
B6L-3-G5-IR	1710	AETSAQVGWQRLMSVMPGHEWSTLDPFYHKLSELLRESGA	11.5	2.0	1.4	1.4	0.7
20E2A-3-A4-IGFR	1711	AGSVTSFYDAMEQLVATGTTSA	16.8	2.5	1.8	1.4	0.7
B6-PD1-IGFR	1712	TDDGFYDALEQLVQGSKK					
20E2-PD1-IGFR (RP10)	1713	GSFYEAQLRLVGGEGKK					

FORMULA 10 (Group 6):

Clone		SEQ ID NO:	Sequence	Ratios over Background			Comparisons	
				E-Tag	IGF-1R	IR	IGF-1R/IR	IR/IGF-1R
R20β-4-E8-IR		1714	VRGFQGGTVMPGYEWLRNAA	41.0	34.9	3.6	9.7	0.1
40F-4-D1-IGFR		1715	LSCLAYSRHGIWRPSTDLGLGRSVGSGSVSTRWRCYDWFE	4.9	4.6	0.3	13.1	0.1
40F-4-B1-IGFR		1716	GLDHSDAVGHVHLGFAWPAQARGWEAGGLEDTWAGYDWL	4.1	3.0	0.2	13.1	0.1
40F-4-D10-IGFR		1717	W.GYAWLS	4.9	4.5	0.4	11.7	0.1

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Besides relative binding at IR or IGF-1R, relative efficacy at the cognate receptor is another important consideration for choosing a potential therapeutic. Thus, a sequence that is efficacious at IR but has little or no significant activity at IGF-1R may also be considered as an important IR therapeutic, irrespective of the relative binding affinities at IR and IGF-1R. For example, A6 selectivity for IR may be enhanced by including glutamic acid in a carboxyl terminal extension at position X₉₅. IR selectivity of the B6 motif may be enhanced by having a tryptophan or phenylalanine at X₁₁. Tryptophan at X₁₃ also favors selectivity of IR. A tryptophan amino acid at X₁₃ rather than leucine at that position also may be used to enhance selectivity for IR. In the reverse B6 motif, a large amino acid at X₁₅ favors IR selectivity. Conversely, small amino acids may confer specificity for IGF-1R. In the F8 motif, an L in position X₂₃ is essentially required for IR binding. In addition, tryptophan at X₃₁ is also highly preferred. At X₃₂, glycine is preferred for IR selectivity.

D. Multiple Binding Sites On IR And IGF-1R

The competition data disclosed herein reveals that at least two separate binding sites are present on IR and IGF-1R which recognize the different sequence motifs provided by this invention.

As shown in Figure 6, competition data indicate that peptides comprising the A6 motifs compete for binding to the same site on IR (Site 1) whereas the D8 motifs compete for a second site (Site 2). The identification of peptides that bind to separate binding sites on IR and IGF-1R provides for various schemes of binding to IR or IGF-1R to increase or decrease its activity. Examples of such schemes for IR are illustrated in Figure 7.

The table below shows sequences based on their groups, which bind to Site 1 or Site 2.

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TABLE 2

REPRESENTATIVE SITE 1 PEPTIDES

A6-like (FYxWF) (SEQ ID NO: 1596):			
5	Clone	Sequence	SEQ ID NO:
	G3	KRGGGTFYEFWFESALRKHGAGKK	1718
	H2	VTFTSAVFHENFYDWFVRQVSCK	1719
	H2C	FHENFYDWFVRQVSCK	1556
	A6S-IR3-E12	GRVDWLQRNANFYDWFVAELG	1560
10	A6S-IR4-G1	NGVERAGTGDNFYDWFVAQLH	1720
	H2CB-R3-B12	QSDSGTVHDFRYGWFRDTWAS	1721
	20E2A-R3-B11	GRFYGWFDQDAIDQLMPWGFDP	1722
	rB6-F6	RYGRWGLAQQFYDWFDR	1723
	E4Dα-1-B8-IR~	GFREGQRWYWFVAQVT	1724
15	H2CA-4-F11-IR	TYKARFLHENFYDWFNRQVSQYFGRV	1725
	H2CB-R3-D2	WTDVDGFGHSGFYRWQNWQER	1726
	H2CB-R3-D12	VASGHVLHGQFYRWFDQFAL	1727
	H2CB-R4-H5	QARVGNVHQQFYEFWFREVMQG	1728
	H2C-B-E8*	TGHRGLGLDEQFYWWFRDALSG	1729
20	H2CB-3-B6-IR~	VGDFCVSHDCFYGWFLRESMQ	1730
	A6S-IR2-C1	RMVFSTGAPQNFYDWFVQEW	1731
B6-like (FYxxLxxL) (SEQ ID NO: 1732):			
	Clone	Sequence	
25	20C11	KDRAFYNGLRDLVGAVYGAWDKK	1733
	20E2	DYKDFYDAIDQLVRGSARAGGTRDKK	1734
	B62-R3-C7	EHWNTVDPPFYFTLFEWLRESG	1735
	B62-R3-C10	EHWNTVDPPFYQYFSELLRESG	1736
30	20E2B-3-B3-IR	AGVNAGFYRYFSTLLDWWDQG	1737
	20E2-B-E3*	IQGWEPFYGWFDVVAQMFE	1738
	20E2A-R4-F9	PPWGARFYDAIEQLVFDNLCC	1739
	RPNN-4-G6-HOLO*	RWPNFYGYFESLLTHFS	1740
	RPNN-4-F3-HOLO*	HYNAFYEYFQVLLAETW	1741
35	20E2A-R4-E2	IGRVRSFYDAIDKLFQSDWER	1742
	RPNN-2-C1-IR*	EGWDFYSYFSGLLASVT	1743
	20E2B-4-F12-IR	SVKEVQFYRYFYDLLQSEESG	1744
	20E2-B-E12	GNSGGSFYRYFQLLLDSDGMS	1745
	20E2A-R3-B6	RDAGSSFYDAIDQLVCLTYFC	1746
40	Reverse B6-like (LxxLxxYF) (SEQ ID NO: 1747):		
	Clone	Sequence	
	rB6-A12	LDALDRLMRYFEERPSL	1748
45	rB6-F9	PLAELWAYFEHSEQGRSSAH	1749
	rB6-4-E7-IR	LDPLDALLQYFWSVPGH	1750
	rB6-4-F9-IR	RRLGSLSTQFYNWFAE	1751
	rB6-E6	ADELEWLLDYFMHQPRP	1752
	rB6-4-F12-IR	DGVLEELFSYFSATVGP	1753
50	Group 6 (WPxYxWL) (SEQ ID NO: 1754):		
	Clone	Sequence	
	R20β-4-A4-IR	WPGYLFEEALQDWRGSTD	1755
55	Peptides by design**:		
	Clone	Sequence	
	H2C-PD1-IR~	AAVHEQFYDWFADQYKK	1756
	A6S-PD1-IR~	QAPSNFYDWFVREWDKK	1757
	20E2-PD1-IR~	QSFYDYIEELLGGEWKK	1758

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B6C-PD1-IR~

DPFYQGLWEWLRESGKK

1759

REPRESENTATIVE SITE 2 PEPTIDES (C-C LOOPS)

5

F8-derived (Long C-C loop):

Clone	Sequence	SEQ ID NO:
F8	HLCVLEELFWGASLFGYCSG	1760
F8-C12	FQSLLEELVWGAPLFRYGTG	1761
10 F8-Des2	PLCVLEELFWGASLFGYCSG	1762
F8-F12	PLCVLEELFWGASLFGQCSG	1763
F8-B9	HLCVLEELFWGASLFGQCSG	1764
15 F8-B12	DLRVLCELFGGAYVLGYCSE	1765
NNKH-2B3	HRSVLKQLSWGASLFGQWAG	1766
NNKH-2F9~	HLVGEELSWWVALLGQWAR	1767
NNKH-4H4~	APVSTEELRWGALLFGQWAG	1768

D8-derived (Small C-C loop):

Clone	Sequence	SEQ ID NO:
D8	KWLDQEWAWVQCEVYGRGCP SKK	1769
D8-G1	QLEEEWAGVQCEVYGRGCP S	1770
D8-B5~	ALEEEWAWVQVRSIRSGLP L	1771
25 D8-A7	SLDQEWAWVQCEVYGRGCL S	1772
D8-F1~	WLEHEWAQIQCELYGRGCT Y	1773

Midi C-C loop:

Clone	Sequence	
30 D8-F10	GLEQGCPWVGLEVQCRGCP S	1774
F8-B12~	DLRVLCELFGGAYVLGYCSE	1775
F8-A9	PLWGLCELFGGASLFGYC S	1776

35 **Based on analysis of entire panning data, amino acid preferences at each position were calculated to define these "idealized" peptides; * Peptides synthesized and currently being purified; ~ Peptides planned.

In various aspects of the present invention, amino acid sequences comprising Site 1 motifs may bind to Site 1 of IR or Site 1 of IGF-1R. Similarly, amino acids sequences comprising Site 2 motifs may bind to Site 2 of IR or Site 2 of IGF-1R. However, specific peptides may show higher binding affinity for IR than for IGF-1R, while other peptides may show higher binding affinity for IGF-1R than for IR. In addition, Site 1 and Site 2 on IR do not "crosstalk", i.e., Site 1-binding sequences do not compete with Site 2-binding sequences at IR. In contrast, Site 1 and Site 2 on IGF-1R do show some crosstalk, suggesting an allosteric effect. These aspects are illustrated in the Examples described hereinbelow.

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E. Multivalent Ligands

This invention provides ligands that preferentially bind different sites on IR and IGF-1R. The A6 amino acid sequence motif confers binding to IR at Site 1 (Figure 6). The D8 amino acid sequence motif confers binding to IR at Site 2 (Figure 6). Accordingly, multimeric ligands may be prepared according to the invention by covalently linking amino acid sequences. Depending on the purpose intended for the multivalent ligand, amino acid sequences that bind the same or different sites may be combined to form a single molecule. Where the multivalent ligand is constructed to bind to the same corresponding site on different receptors, or different subunits of a receptor, the amino acid sequences of the ligand for binding to the receptors may be the same or different, provided that if different amino acid sequences are used, they both bind to the same site.

Multivalent ligands may be prepared by either expressing amino acid sequences which bind to the individual sites separately and then covalently linking them together, or by expressing the multivalent ligand as a single amino acid sequence which comprises within it the combination of specific amino acid sequences for binding.

Various combinations of amino acid sequences may be combined to produce multivalent ligands having specific desirable properties. Thus, agonists may be combined with agonists, antagonists combined with antagonists, and agonists combined with antagonists. Combining amino acid sequences that bind to the same site to form a multivalent ligand may be useful to produce molecules that are capable of cross-linking together multiple receptor units. Multivalent ligands may also be constructed to combine amino acid sequences which bind to different sites (Figure 7).

In view of the discovery disclosed herein of monomers having agonist properties at IR or IGF-1R, preparation of multivalent ligands may be useful to prepare ligands having more desirable pharmacokinetic properties due to the presence of multiple bind sites on a single molecule. In addition, combining amino acid sequences that bind to different sites with different

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affinities provides a means for modulating the overall potency and affinity of the ligand for IR or IGF-1R.

1. Construction of Hybrids

In one embodiment, hybrids of at least two peptides (e.g., dimer
5 peptides) may be produced as recombinant fusion polypeptides, which are expressed in any suitable expression system. The polypeptides may bind the receptor as either fusion constructs containing amino acid sequences besides the ligand binding sequences or as cleaved proteins from which signal sequences or other sequences unrelated to ligand binding are
10 removed. Sequences for facilitating purification of the fusion protein may also be expressed as part of the construct. Such sequences optionally may be subsequently removed to produce the mature binding ligand. Recombinant expression also provides means for producing large quantities of ligand. In addition, recombinant expression may be used to express
15 different combinations of amino acid sequences and to vary the orientation of their combination, i.e., amino to carboxyl terminal orientation.

In one embodiment shown below (Figure 28), MBP-FLAG®-
PEPTIDE-(GGS)_n (SEQ ID NO: 1777)-PEPTIDE-E-TAG, a fusion construct
20 producing a peptide dimer comprises a maltose binding protein amino acid sequence (MBP) or similar sequence useful for enabling the affinity chromatography purification of the expressed peptide sequences. This purification facilitating sequence may then be attached to a FLAG® sequence to provide a cleavage site to remove the initial sequence. The dimer then follows which includes the intervening linker and a tag sequence
25 may be included at the carboxyl terminal portion to facilitate identification/purification of the expression of peptide. In the representative construct illustrated above, G and S are glycine and serine residues, which make up the linker sequence. As non-limiting examples, n can be 1, 2, 3, or 4 to yield a linker sequence of 3, 6, 9, and 12 amino acids, respectively.

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In addition to producing the dimer peptides by recombinant protein expression, dimer peptides may also be produced by peptide synthesis whereby a synthetic technique such as Merrifield synthesis (Merrifield, 1997), may be used to construct the entire peptide.

5 Other methods of constructing dimer peptides include introducing a linker molecule that activates the terminal end of a peptide so that it can covalently bind to a second peptide. Examples of such linkers include, but are not limited to, diaminopropionic acid activated with an oxyamino function. A preferred linker is a dialdehyde having the formula $O=CH-(CH_2)_n-CH=O$, wherein n is at least 2 to 6, but is preferably 6 to produce a
10 linker of about 25 to 30 angstroms in length. Other preferred linkers are shown in Table 3. Linkers may be used, for example, to couple monomers at either the carboxyl terminal or the amino terminal ends to form dimer peptides. Also, the chemistry can be inverted, i.e., the peptides to be
15 coupled can be equipped with aldehyde functions, either by oxidation with sodium periodate of an N-terminal serine, or by oxidation of any other vicinal hydroxy- or amino-groups, and the linker can comprise two oxyamino functions (e.g., at end of a polyethylene glycol linker) or amino groups which are coupled by reductive amination.

20 In specific embodiments, Site 1-Site 2 and Site 2-Site 1 orientations are possible. In addition, N-terminal to N-terminal (N-N); C-terminal to C-terminal (C-C); N-terminal to C-terminal (N-C); and C-terminal to N-terminal (C-N) linkages are possible. Accordingly, peptides may be oriented Site 1 to Site 2, or Site 2 to Site 1, and may be linked N-terminus to N-terminus, C-
25 terminus to C-terminus, N-terminus to C-terminus, or C-terminus to N-terminus. In certain cases, a specific orientation may be preferable to others, for example, for maximal agonist or antagonist activity.

In an unexpected and surprising result, the orientation and linkage of the monomer subunits has been found to dramatically alter dimer activity
30 (see Examples, below). In particular, certain Site 1/Site 2 heterodimer sequences show agonist or antagonist activity at IR, depending on

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orientation and linkage of the constituent monomer subunits. For example, a Site 1-Site 2 orientation (C-N linkage), e.g., the S453 heterodimer, shows antagonist activity at IR (Figure 18A; Table 7). In contrast, a Site 2-Site 1 orientation (C-N linkage), e.g., the S455 heterodimer, shows potent agonist activity at IR (Figure 18D; Table 7). Similarly, Site 1-Site 2 (C-N linkage) heterodimers, e.g., S425 and S459, show antagonist activity at IR (Table 7), while Site 1-Site 2 (C-C or N-N linkage) heterodimers, e.g., S432-S438, S454, and S456, show agonist activity (Table 7).

Whether produced by recombinant gene expression or by conventional chemical linkage technology, the various amino acid sequences may be coupled through linkers of various lengths. Where linked sequences are expressed recombinantly, and based on an average amino acid length of about 4 angstroms, the linkers for connecting the two amino acid sequences would typically range from about 3 to about 12 amino acids corresponding to from about 12 to about 48 Å. Accordingly, the preferred distance between binding sequences is from about 2 to about 50 Å. More preferred is 4 to about 40. The degree of flexibility of the linker between the amino acid sequences may be modulated by the choice of amino acids used to construct the linker. The combination of glycine and serine is useful for producing a flexible, relatively unrestrictive linker. A more rigid linker may be constructed by using amino acids with more complex side chains within the linkage sequence.

2. Characterization Of Specific Dimers

Specific dimers which are comprised of monomer subunits that both bind with high affinity to the same site on IR (i.e., homodimers), or monomer subunits that bind to different sites on IR (i.e., heterodimers) are disclosed herein.

Other combinations of peptides are within the scope of this invention and may be determined as demonstrated in the examples described herein.

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F. Peptide Synthesis

Many conventional techniques in molecular biology, protein biochemistry, and immunology may be used to produce the amino acid sequences for use with this invention. The present invention encompasses
5 the specific amino acid sequences shown in Figures 1-4, 8, and 9 and Table 7, *inter alia*, without additions (e.g., linker or spacer sequences) deletions, alterations, or modification. The present invention further encompasses variants that include additional sequences, altered sequences, and functional fragments thereof. In a preferred embodiment, the amino acid
10 sequence variant or fragment shares at least one function characteristic (e.g., binding, agonist, or antagonist activity) of the reference sequence. Variant peptides include, for example, genetically engineered mutants, and may differ from the amino acid sequences shown in the figures and tables of the application by the addition, deletion, or substitution of one or more
15 amino acid residues. Alterations may occur at the amino- or carboxy-terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among the amino acids in the reference sequence or in one or more contiguous groups within the reference sequence. In addition, variants may comprise synthetic
20 or non-naturally occurring amino acids in accordance with this invention.

Variant amino acid sequences can have conservative changes, wherein a substituted amino acid has similar structural or chemical properties, e.g., replacement of leucine with isoleucine. More infrequently, a variant peptide can have non-conservative changes, e.g., substitution of a
25 glycine with a tryptophan. Guidance in determining which amino acid residues can be substituted, inserted, or deleted without abolishing binding or biological activity can be found using computer programs well known in the art, for example, DNASTAR software (DNASTAR, Inc., Madison, WI). Guidance is also provided by the data disclosed herein. In particular,
30 Figures 1-4, 8, 9, 43, 44, and Table 7, *inter alia*, teach which amino acid residues can be deleted, added, substituted, or modified, while maintaining

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the IR- or IGF-1R-related function(s) (e.g., binding, agonist, or antagonist activity) of the amino acid sequences.

For the purposes of this invention, the amino acids are grouped as follows: amino acids possessing alcohol groups are serine (S) and
5 threonine (T). Aliphatic amino acids are isoleucine (I), leucine (L), valine (V), and methionine (M). Aromatic amino acids are phenylalanine (F), histidine (H), tryptophan (W), and tyrosine (Y). Hydrophobic amino acids are alanine (A), cysteine (C), phenylalanine (F), glycine (G), histidine (H), isoleucine (I), leucine (L), methionine (M), arginine (R), threonine (T), valine
10 (V), tryptophan (W), and tyrosine (Y). Negative amino acids are aspartic acid (D) and glutamic acid (E). The following amino acids are polar amino acids: cysteine (C), aspartic acid (D), glutamic acid (E), histidine (H), lysine (K), asparagine (N), glutamine (Q), arginine (R), serine (S), and threonine (T). Positive amino acids are histidine (H), lysine (K), and arginine (R).
15 Small amino acids are alanine (A), cysteine (C), aspartic acid (D), glycine (G), asparagine (N), proline (P), serine (S), threonine (T), and valine (V). Very small amino acids are alanine (A), glycine (G) and serine (S). Amino acids likely to be involved in a turn formation are alanine (A), cysteine (C), aspartic acid (D), glutamic acid (E), glycine (G), histidine (H), lysine (K),
20 asparagine (N), glutamine (Q), arginine (R), serine (S), proline (P), and threonine (T). As non-limiting examples, the amino acids within each of these defined groups may be substituted for each other in the formulas described above, as conservative substitutions, subject to the specific preferences stated herein.

25 Substantial changes in function can be made by selecting substitutions that are less conservative than those shown in the defined groups, above. For example, non-conservative substitutions can be made which more significantly affect the structure of the peptide in the area of the alteration, for example, the alpha-helical, or beta-sheet structure; the charge
30 or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which generally are expected to produce the

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greatest changes in the peptide's properties are those where 1) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl, or alanyl; 2) a cysteine or proline is substituted for (or by) any other residue; 3) a residue
5 having an electropositive side chain, e.g., lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or 4) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) a residue that does not have a side chain, e.g., glycine.

Amino acid preferences have been identified for certain peptides and
10 peptide groups of the present invention. For example, amino acid preferences for the RP9, D8, and Group 6 (Formula 10) peptides are shown in Tables 17-19, below.

Variants also include amino acid sequences in which one or more residues are modified (i.e., by phosphorylation, sulfation, acylation, PEGylation, etc.), and mutants comprising one or more modified residues.
15 Amino acid sequences may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotope, fluorescent, and enzyme labels. Fluorescent labels include, for example, Cy3, Cy5, Alexa, BODIPY, fluorescein (e.g., FluorX, DTAF, and FITC), rhodamine (e.g., TRITC), auramine, Texas Red, AMCA
20 blue, and Lucifer Yellow. Preferred isotope labels include ³H, ¹⁴C, ³²P, ³⁵S, ³⁶Cl, ⁵¹Cr, ⁵⁷Co, ⁵⁸Co, ⁵⁹Fe, ⁹⁰Y, ¹²⁵I, ¹³¹I, and ¹⁸⁶Re. Preferred enzyme labels include peroxidase, β -glucuronidase, β -D-glucosidase, β -D-galactosidase, urease, glucose oxidase plus peroxidase, and alkaline
25 phosphatase (see, e.g., U.S. Pat. Nos. 3,654,090; 3,850,752 and 4,016,043). Enzymes can be conjugated by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde, and the like. Enzyme labels can be detected visually, or measured by calorimetric, spectrophotometric, fluorospectrophotometric, amperometric, or gasometric
30 techniques. Other labeling systems, such as avidin/biotin, Tyramide Signal Amplification (TSA™), are known in the art, and are commercially available

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(see, e.g., ABC kit, Vector Laboratories, Inc., Burlingame, CA; NEN® Life Science Products, Inc., Boston, MA).

1. Recombinant Synthesis of Peptides

To obtain recombinant peptides, DNA sequences encoding these
5 peptides may be cloned into any suitable vectors for expression in intact host cells or in cell-free translation systems by methods well known in the art (see Sambrook *et al.*, 1989). The particular choice of the vector, host, or translation system is not critical to the practice of the invention.

A large number of vectors, including bacterial, yeast, and mammalian
10 vectors, have been described for replication and/or expression in various host cells or cell-free systems, and may be used for gene therapy as well as for simple cloning or protein expression. In one aspect of the present invention, an expression vector comprises a nucleic acid encoding a IR or IGF-1R agonist or antagonist peptide, as described herein, operably linked
15 to at least one regulatory sequence. Regulatory sequences are known in the art and are selected to direct expression of the desired protein in an appropriate host cell. Accordingly, the term regulatory sequence includes promoters, enhancers and other expression control elements (see D.V. Goeddel (1990) *Methods Enzymol.* **185**:3-7). Enhancer and other
20 expression control sequences are described in *Enhancers and Eukaryotic Gene Expression*, Cold Spring Harbor Press, Cold Spring Harbor, NY (1983). It should be understood that the design of the expression vector may depend on such factors as the choice of the host cell to be transfected and/or the type of peptide desired to be expressed.

25 Several regulatory elements (e.g., promoters) have been isolated and shown to be effective in the transcription and translation of heterologous proteins in the various hosts. Such regulatory regions, methods of isolation, manner of manipulation, etc. are known in the art. Non-limiting examples of bacterial promoters include the β -lactamase (penicillinase) promoter; lactose
30 promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter;

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lambda-derived P₁ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include the 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactose epimerase promoter, and alcohol dehydrogenase (ADH1) promoter. Suitable promoters for mammalian cells include, without limitation, viral promoters, such as those from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Preferred replication and inheritance systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, CEN ARS, 2 μ m ARS and the like. While expression vectors may replicate autonomously, they may also replicate by being inserted into the genome of the host cell, by methods well known in the art.

To obtain expression in eukaryotic cells, terminator sequences, polyadenylation sequences, and enhancer sequences that modulate gene expression may be required. Sequences that cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or preprotein or proprotein sequences, may also be included. These sequences are well described in the art. DNA sequences can be optimized, if desired, for more efficient expression in a given host organism or expression system. For example, codons can be altered to conform to the preferred codon usage in a given host cell or cell-free translation system using well-established techniques.

Codon usage data can be obtained from publicly-available sources, for example, the Codon Usage Database at <http://www.kazusa.or.jp/codon/>. In addition, computer programs that translate amino acid sequence information into nucleotide sequence information in accordance with codon preferences (i.e., backtranslation programs) are widely available. See, for example, Backtranslate program from Genetics Computer Group (GCG),

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Accelrys, Inc., Madison, WI; and Backtranslation Applet from Entelechon GmbH, Regensburg, Germany. Thus, using the peptide sequences disclosed herein, one of ordinary skill in the art can design nucleic acids to yield optimal expression levels in the translation system or host cell of
5 choice.

Expression and cloning vectors will likely contain a selectable marker, a gene encoding a protein necessary for survival or growth of a host cell transformed with the vector. The presence of this gene ensures growth of only those host cells that express the inserts. Typical selection genes
10 encode proteins that 1) confer resistance to antibiotics or other toxic substances, e.g., ampicillin, neomycin, methotrexate, etc.; 2) complement auxotrophic deficiencies, or 3) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*. Markers may be an inducible or non-inducible gene and will generally allow
15 for positive selection. Non-limiting examples of markers include the ampicillin resistance marker (i.e., beta-lactamase), tetracycline resistance marker, neomycin/kanamycin resistance marker (i.e., neomycin phosphotransferase), dihydrofolate reductase, glutamine synthetase, and the like. The choice of the proper selectable marker will depend on the host
20 cell, and appropriate markers for different hosts as understood by those of skill in the art.

Suitable expression vectors for use with the present invention include, but are not limited to, pUC, pBluescript (Stratagene), pET (Novagen, Inc., Madison, WI), and pREP (Invitrogen) plasmids. Vectors can
25 contain one or more replication and inheritance systems for cloning or expression, one or more markers for selection in the host, e.g., antibiotic resistance, and one or more expression cassettes. The inserted coding sequences can be synthesized by standard methods, isolated from natural sources, or prepared as hybrids. Ligation of the coding sequences to
30 transcriptional regulatory elements (e.g., promoters, enhancers, and/or

insulators) and/or to other amino acid encoding sequences can be carried out using established methods.

Suitable cell-free expression systems for use with the present invention include, without limitation, rabbit reticulocyte lysate, wheat germ
5 extract, canine pancreatic microsomal membranes, *E. coli* S30 extract, and coupled transcription/translation systems (Promega Corp., Madison, WI). These systems allow the expression of recombinant peptides upon the addition of cloning vectors, DNA fragments, or RNA sequences containing protein-coding regions and appropriate promoter elements.

10 Non-limiting examples of suitable host cells include bacteria, archaea, insect, fungi (e.g., yeast), plant, and animal cells (e.g., mammalian, especially human). Of particular interest are *Escherichia coli*, *Bacillus subtilis*, *Saccharomyces cerevisiae*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and immortalized mammalian myeloid and lymphoid cell lines.
15 Techniques for the propagation of mammalian cells in culture are well-known (see, Jakoby and Pastan (Eds), 1979, *Cell Culture. Methods in Enzymology*, volume 58, Academic Press, Inc., Harcourt Brace Jovanovich, NY). Examples of commonly used mammalian host cell lines are VERO and HeLa cells, CHO cells, and WI38, BHK, and COS cell lines, although it will
20 be appreciated by the skilled practitioner that other cell lines may be used, e.g., to provide higher expression, or other features.

Host cells can be transformed, transfected, or infected as appropriate by any suitable method including electroporation, calcium chloride-, lithium chloride-, lithium acetate/polyethylene glycol-, calcium phosphate-, DEAE-
25 dextran-, liposome-mediated DNA uptake, spheroplasting, injection, microinjection, microprojectile bombardment, phage infection, viral infection, or other established methods. Alternatively, vectors containing the nucleic acids of interest can be transcribed *in vitro*, and the resulting RNA introduced into the host cell by well-known methods, e.g., by injection (see,
30 Kubo *et al.*, 1988, *FEBS Letts.* **241**:119). The cells into which have been

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introduced nucleic acids described above are meant to also include the progeny of such cells.

Nucleic acids encoding the peptides of the invention may be isolated directly from recombinant phage libraries (e.g., RAPIDLIB® or GRABLIB® libraries) described herein. Alternatively, the polymerase chain reaction (PCR) method can be used to produce nucleic acids of the invention, using the recombinant phage libraries as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

Nucleic acids encoding the peptides of the present invention can also be produced by chemical synthesis, e.g., by the phosphoramidite method described by Beaucage *et al.*, 1981, *Tetra. Letts.* **22**:1859-1862, or the triester method according to Matteucci *et al.*, 1981, *J. Am. Chem. Soc.*, **103**:3185, and can be performed on commercial, automated oligonucleotide synthesizers. A double-stranded fragment may be obtained from the single-stranded product of chemical synthesis either by synthesizing the complementary strand and annealing the strands together under appropriate conditions or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The nucleic acids encoding the peptides of the invention can be produced in large quantities by replication in a suitable host cell. Natural or synthetic nucleic acid fragments, comprising at least ten contiguous bases coding for a desired amino acid sequence can be incorporated into recombinant nucleic acid constructs, usually DNA constructs, capable of introduction into and replication in a prokaryotic or eukaryotic cell. Usually the nucleic acid constructs will be suitable for replication in a unicellular host, such as yeast or bacteria, but may also be intended for introduction to (with and without integration within the genome) cultured mammalian or plant or other eukaryotic cells, cell lines, tissues, or organisms. The purification of nucleic acids produced by the methods of the present

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invention is described, for example, in Sambrook *et al.*, 1989; F.M. Ausubel *et al.*, 1992, *Current Protocols in Molecular Biology*, J. Wiley and Sons, New York, NY.

These nucleic acids can encode variant or truncated forms of the peptides as well as the reference peptides shown in Figures 1-4, 8, and 9 and Table 7, *inter alia*. Large quantities of the nucleic acids and peptides of the present invention may be prepared by expressing the nucleic acids or portions thereof in vectors or other expression vehicles in compatible prokaryotic or eukaryotic host cells. The most commonly used prokaryotic hosts are strains of *Escherichia coli*, although other prokaryotes, such as *Bacillus subtilis* or *Pseudomonas* may also be used. Mammalian or other eukaryotic host cells, such as those of yeast, filamentous fungi, plant, insect, or amphibian or avian species, may also be useful for production of the proteins of the present invention. For example, insect cell systems (i.e., lepidopteran host cells and baculovirus expression vectors) are particularly suited for large-scale protein production.

Host cells carrying an expression vector (i.e., transformants or clones) are selected using markers depending on the mode of the vector construction. The marker may be on the same or a different DNA molecule, preferably the same DNA molecule. In prokaryotic hosts, the transformant may be selected, e.g., by resistance to ampicillin, tetracycline or other antibiotics. Production of a particular product based on temperature sensitivity may also serve as an appropriate marker.

For some purposes, it is preferable to produce the peptide in a recombinant system in which the peptide contains an additional sequence (e.g., epitope or protein) tag that facilitates purification. Non-limiting examples of epitope tags include c-myc, haemagglutinin (HA), polyhistidine (6X-HIS)(SEQ ID NO: 1778), GLU-GLU, and DYKDDDDK (SEQ ID NO:1779) or DYKD (SEQ ID NO:1545; FLAG®) epitope tags. Non-limiting examples of protein tags include glutathione-S-transferase (GST), green fluorescent protein (GFP), and maltose binding protein (MBP). In one

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approach, the coding sequence of a peptide can be cloned into a vector that creates a fusion with a sequence tag of interest. Suitable vectors include, without limitation, pRSET (Invitrogen Corp., San Diego, CA), pGEX (Amersham Pharmacia Biotech, Inc., Piscataway, NJ), pEGFP (CLONTECH Laboratories, Inc., Palo Alto, CA), and pMAL™ (New England BioLabs, Inc., Beverly, MA) plasmids. Following expression, the epitope or protein tagged peptide can be purified from a crude lysate of the translation system or host cell by chromatography on an appropriate solid-phase matrix. In some cases, it may be preferable to remove the epitope or protein tag (i.e., via protease cleavage) following purification.

Methods for directly purifying peptides from sources such as cellular or extracellular lysates are well known in the art (see Harris and Angal, 1989). Such methods include, without limitation, sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE), preparative disc-gel electrophoresis, isoelectric focusing, high-performance liquid chromatography (HPLC), reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, countercurrent distribution, and combinations thereof. Peptides can be purified from many possible sources, for example, plasma, body tissues, or body fluid lysates derived from human or animal, including mammalian, bird, fish, and insect sources.

Antibody-based methods may also be used to purify peptides. Antibodies that recognize these peptides or fragments derived therefrom can be produced and isolated. The peptide can then be purified from a crude lysate by chromatography on an antibody-conjugated solid-phase matrix (see Harlow and Lane, 1998).

2. Chemical Synthesis Of Peptides

Alternately, peptides may be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The peptides are preferably prepared by solid-

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phase peptide synthesis; for example, as described by Merrifield (1965; 1997).

According to methods known in the art, peptides can be chemically synthesized by commercially available automated procedures, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation, classical solution synthesis. In addition, recombinant and synthetic methods of peptide production can be combined to produce semi-synthetic peptides. The peptides of the invention are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* **85**:2149; 1997. In one embodiment, synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the peptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

The alpha-amino protecting groups are those known to be useful in the art of stepwise peptide synthesis. Included are acyl type protecting groups, e.g., formyl, trifluoroacetyl, acetyl, aromatic urethane type protecting groups, e.g., benzyloxycarbonyl (Cbz), substituted benzyloxycarbonyl and 9-fluorenylmethyloxycarbonyl (Fmoc), aliphatic urethane protecting groups, e.g., t-butyloxycarbonyl (Boc), isopropyloxycarbonyl, cyclohexyloxycarbonyl, and alkyl type protecting groups, e.g., benzyl, triphenylmethyl. The preferred protecting group is Boc. The side-chain protecting groups for Tyr include tetrahydropyranyl, tert-butyl, trityl, benzyl, Cbz, 4-Br-Cbz and 2,6-dichlorobenzyl. The preferred side-chain protecting group for Tyr is 2,6-dichlorobenzyl. The side-chain protecting groups for Asp include benzyl, 2,6-dichlorobenzyl, methyl, ethyl, and cyclohexyl. The preferred side-chain protecting group for Asp is cyclohexyl. The side-chain protecting groups for Thr and Ser include acetyl, benzoyl, trityl, tetrahydropyranyl, benzyl, 2,6-

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dichlorobenzyl, and Cbz. The preferred protecting group for Thr and Ser is benzyl. The side-chain protecting groups for Arg include nitro, Tos, Cbz, adamantyloxycarbonyl, and Boc. The preferred protecting group for Arg is Tos. The side-chain amino group of Lys can be protected with Cbz, 2-Cl-Cbz, Tos, or Boc. The 2-Cl-Cbz group is the preferred protecting group for Lys.

The side-chain protecting groups selected must remain intact during coupling and not be removed during the deprotection of the amino-terminus protecting group or during coupling conditions. The side-chain protecting groups must also be removable upon the completion of synthesis, using reaction conditions that will not alter the finished peptide.

Solid phase synthesis is usually carried out from the carboxy-terminus by coupling the alpha-amino protected (side-chain protected) amino acid to a suitable solid support. An ester linkage is formed when the attachment is made to a chloromethyl or hydroxymethyl resin, and the resulting peptide will have a free carboxyl group at the C-terminus. Alternatively, when a benzhydrylamine or p-methylbenzhydrylamine resin is used, an amide bond is formed and the resulting peptide will have a carboxamide group at the C-terminus. These resins are commercially available, and their preparation has described by Stewart *et al.*, 1984, *Solid Phase Peptide Synthesis* (2nd Edition), Pierce Chemical Co., Rockford, IL.

The C-terminal amino acid, protected at the side chain if necessary and at the alpha-amino group, is coupled to the benzhydrylamine resin using various activating agents including dicyclohexylcarbodiimide (DCC), N,N'-diisopropyl-carbodiimide and carbonyldiimidazole. Following the attachment to the resin support, the alpha-amino protecting group is removed using trifluoroacetic acid (TFA) or HCl in dioxane at a temperature between 0 and 25°C. Dimethylsulfide is added to the TFA after the introduction of methionine (Met) to suppress possible S-alkylation. After removal of the alpha-amino protecting group, the remaining protected amino acids are coupled stepwise in the required order to obtain the desired sequence.

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Various activating agents can be used for the coupling reactions including DCC, N,N'-diisopropyl-carbodiimide, benzotriazol-1-yl-oxy-tris-(dimethylamino) phosphonium hexa-fluorophosphate (BOP) and DCC-hydroxybenzotriazole (HOBt). Each protected amino acid is used in excess
5 (>2.0 equivalents), and the couplings are usually carried out in N-methylpyrrolidone (NMP) or in DMF, CH₂Cl₂ or mixtures thereof. The extent of completion of the coupling reaction is monitored at each stage, e.g., by the ninhydrin reaction as described by Kaiser *et al.*, 1970, *Anal. Biochem.* **34**:595. In cases where incomplete coupling is found, the
10 coupling reaction is repeated. The coupling reactions can be performed automatically with commercially available instruments.

After the entire assembly of the desired peptide, the peptide-resin is cleaved with a reagent such as liquid HF for 1-2 hours at 0°C, which cleaves the peptide from the resin and removes all side-chain protecting groups. A
15 scavenger such as anisole is usually used with the liquid HF to prevent cations formed during the cleavage from alkylating the amino acid residues present in the peptide. The peptide-resin can be deprotected with TFA/dithioethane prior to cleavage if desired.

Side-chain to side-chain cyclization on the solid support requires the
20 use of an orthogonal protection scheme which enables selective cleavage of the side-chain functions of acidic amino acids (e.g., Asp) and the basic amino acids (e.g., Lys). The 9-fluorenylmethyl (Fm) protecting group for the side-chain of Asp and the 9-fluorenylmethyloxycarbonyl (Fmoc) protecting group for the side-chain of Lys can be used for this purpose. In these
25 cases, the side-chain protecting groups of the Boc-protected peptide-resin are selectively removed with piperidine in DMF. Cyclization is achieved on the solid support using various activating agents including DCC, DCC/HOBt, or BOP. The HF reaction is carried out on the cyclized peptide-resin as described above.

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3. Peptide Libraries

Peptide libraries produced and screened according to the present invention are useful in providing new ligands for IR and IGF-1R. Peptide libraries can be designed and panned according to methods described in detail herein, and methods generally available to those in the art (see, e.g.,
5 U.S. Patent No. 5,723,286 issued March 3, 1998 to Dower *et al.*). In one aspect, commercially available phage display libraries can be used (e.g., RAPIDLIB® or GRABLIB®, DGI BioTechnologies, Inc., Edison, NJ; Ph.D. C7C Disulfide Constrained Peptide Library, New England Biolabs). In
10 another aspect, an oligonucleotide library can be prepared according to methods known in the art, and inserted into an appropriate vector for peptide expression. For example, vectors encoding a bacteriophage structural protein, preferably an accessible phage protein, such as a bacteriophage coat protein, can be used. Although one skilled in the art will appreciate that
15 a variety of bacteriophage may be employed in the present invention, in preferred embodiments the vector is, or is derived from, a filamentous bacteriophage, such as, for example, f1, fd, Pf1, M13, etc. In particular, the fd-tet vector has been extensively described in the literature (see, e.g., Zacher *et al.*, 1980, *Gene* 9:127-140; Smith *et al.*, 1985, *Science* 228:1315-
20 1317; Parmley and Smith, 1988, *Gene* 73:305-318).

The phage vector is chosen to contain or is constructed to contain a cloning site located in the 5' region of the gene encoding the bacteriophage structural protein, so that the peptide is accessible to receptors in an affinity enrichment procedure as described hereinbelow. The structural phage
25 protein is preferably a coat protein. An example of an appropriate coat protein is pIII. A suitable vector may allow oriented cloning of the oligonucleotide sequences that encode the peptide so that the peptide is expressed at or within a distance of about 100 amino acid residues of the N-terminus of the mature coat protein. The coat protein is typically expressed
30 as a preprotein, having a leader sequence.

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Thus, desirably the oligonucleotide library is inserted so that the N-terminus of the processed bacteriophage outer protein is the first residue of the peptide, i.e., between the 3'-terminus of the sequence encoding the leader protein and the 5'-terminus of the sequence encoding the mature protein or a portion of the 5' terminus. The library is constructed by cloning
5 an oligonucleotide which contains the variable region of library members (and any spacers, as discussed below) into the selected cloning site. Using known recombinant DNA techniques (see generally, Sambrook *et al.*, 1989, *Molecular Cloning, A Laboratory Manual*, 2d ed., Cold Spring Harbor
10 Laboratory Press, Cold Spring Harbor, N.Y., 1989), an oligonucleotide may be constructed which, *inter alia*; 1) removes unwanted restriction sites and adds desired ones; 2) reconstructs the correct portions of any sequences which have been removed (such as a correct signal peptidase site, for example); 3) inserts the spacer residues, if any; and/or 4) corrects the
15 translation frame (if necessary) to produce active, infective phage.

The central portion of the oligonucleotide will generally contain one or more IR and/or IGF-1R binding sequences and, optionally, spacer sequences. The sequences are ultimately expressed as peptides (with or without spacers) fused to or in the N-terminus of the mature coat protein on
20 the outer, accessible surface of the assembled bacteriophage particles. The size of the library will vary according to the number of variable codons, and hence the size of the peptides, which are desired. Generally the library will be at least about 10^6 members, usually at least 10^7 , and typically 10^8 or more members. To generate the collection of oligonucleotides which forms
25 a series of codons encoding a random collection of amino acids and which is ultimately cloned into the vector, a codon motif is used, such as $(NNK)_x$, where N may be A, C, G, or T (nominally equimolar), K is G or T (nominally equimolar), and x is typically up to about 5, 6, 7, 8, or more, thereby producing libraries of penta-, hexa-, hepta-, and octa-peptides or larger.
30 The third position may also be G or C, designated "S". Thus, NNK or NNS

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1) code for all the amino acids; 2) code for only one stop codon; and 3) reduce the range of codon bias from 6:1 to 3:1.

It should be understood that, with longer peptides, the size of the library that is generated may become a constraint in the cloning process.

5 The expression of peptides from randomly generated mixtures of oligonucleotides in appropriate recombinant vectors is known in the art (see, e.g., Oliphant *et al.*, Gene **44**:177-183). For example, the codon motif (NNK)₆ produces 32 codons, one for each of 12 amino acids, two for each of five amino acids, three for each of three amino acids and one (amber) stop
10 codon. Although this motif produces a codon distribution as equitable as available with standard methods of oligonucleotide synthesis, it results in a bias against peptides containing one-codon residues. In particular, a complete collection of hexacodons contains one sequence encoding each peptide made up of only one-codon amino acids, but contains 729 (3⁶)
15 sequences encoding each peptide with only three-codon amino acids.

An alternative approach to minimize the bias against one-codon residues involves the synthesis of 20 activated trinucleotides, each representing the codon for one of the 20 genetically encoded amino acids. These are synthesized by conventional means, removed from the support
20 while maintaining the base and 5-OH-protecting groups, and activated by the addition of 3'-O-phosphoramidite (and phosphate protection with *b*-cyanoethyl groups) by the method used for the activation of mononucleosides (see, generally, McBride and Caruthers, 1983, *Tetrahedron Letters* **22**:245). Degenerate oligocodons are prepared using
25 these trimers as building blocks. The trimers are mixed at the desired molar ratios and installed in the synthesizer. The ratios will usually be approximately equimolar, but may be a controlled unequal ratio to obtain the over- to under-representation of certain amino acids coded for by the degenerate oligonucleotide collection. The condensation of the trimers to
30 form the oligocodons is done essentially as described for conventional synthesis employing activated mononucleosides as building blocks (see,

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e.g., Atkinson and Smith, 1984, *Oligonucleotide Synthesis*, M.J. Gait, Ed., p. 35-82). This procedure generates a population of oligonucleotides for cloning that is capable of encoding an equal distribution (or a controlled unequal distribution) of the possible peptide sequences. Advantageously,
5 this approach may be employed in generating longer peptide sequences, since the range of bias produced by the (NNK)₆ motif increases by three-fold with each additional amino acid residue.

When the codon motif is (NNK)_x, as defined above, and when x equals 8, there are 2.6×10^{10} possible octa-peptides. A library containing
10 most of the octa-peptides may be difficult to produce. Thus, a sampling of the octa-peptides may be accomplished by constructing a subset library using up to about 10% of the possible sequences, which subset of recombinant bacteriophage particles is then screened. If desired, to extend the diversity of a subset library, the recovered phage subset may be
15 subjected to mutagenesis and then subjected to subsequent rounds of screening. This mutagenesis step may be accomplished in two general ways: the variable region of the recovered phage may be mutagenized, or additional variable amino acids may be added to the regions adjoining the initial variable sequences.

20 To diversify around active peptides (i.e., binders) found in early rounds of panning, the positive phage can be sequenced to determine the identity of the active peptides. Oligonucleotides can then be synthesized based on these peptide sequences. The syntheses are done with a low level of all bases incorporated at each step to produce slight variations of
25 the primary oligonucleotide sequences. This mixture of (slightly) degenerate oligonucleotides can then be cloned into the affinity phage by methods known to those in the art. This method produces systematic, controlled variations of the starting peptide sequences as part of a secondary library. It requires, however, that individual positive phage be sequenced before
30 mutagenesis, and thus is useful for expanding the diversity of small numbers of recovered phage.

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An alternate approach to diversify the selected phage allows the mutagenesis of a pool, or subset, of recovered phage. In accordance with this approach, phage recovered from panning are pooled and single stranded DNA is isolated. The DNA is mutagenized by treatment with, e.g.,
5 nitrous acid, formic acid, or hydrazine. These treatments produce a variety of damage to the DNA. The damaged DNA is then copied with reverse transcriptase, which misincorporates bases when it encounters a site of damage. The segment containing the sequence encoding the receptor-binding peptide is then isolated by cutting with restriction nuclease(s)
10 specific for sites flanking the peptide coding sequence. This mutagenized segment is then recloned into undamaged vector DNA, the DNA is transformed into cells, and a secondary library according to known methods. General mutagenesis methods are known in the art (see Myers *et al.*, 1985, *Nucl. Acids Res.* **13**:3131-3145; Myers *et al.*, 1985, *Science* **229**:242-246; Myers, 1989, *Current Protocols in Molecular Biology Vol. 1*, 8.3.1-8.3.6, F. Ausubel *et al.*, eds, J. Wiley and Sons, New York).

In another general approach, the addition of amino acids to a peptide or peptides found to be active, can be carried out using various methods. In one, the sequences of peptides selected in early panning are determined
20 individually and new oligonucleotides, incorporating the determined sequence and an adjoining degenerate sequence, are synthesized. These are then cloned to produce a secondary library. Alternatively, methods can be used to add a second IR or IGF-1R binding sequence to a pool of peptide-bearing phage. In accordance with one method, a restriction site is
25 installed next to the first IR or IGF-1R binding sequence. Preferably, the enzyme should cut outside of its recognition sequence. The recognition site may be placed several bases from the first binding sequence. To insert a second IR or IGF-1R binding sequence, the pool of phage DNA is digested and blunt-ended by filling in the overhang with Klenow fragment. Double-
30 stranded, blunt-ended, degenerately synthesized oligonucleotides are then ligated into this site to produce a second binding sequence juxtaposed to the

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first binding sequence. This secondary library is then amplified and screened as before.

While in some instances it may be appropriate to synthesize longer peptides to bind certain receptors, in other cases it may be desirable to provide peptides having two or more IR or IGF-1R binding sequences separated by spacer (e.g., linker) residues. For example, the binding sequences may be separated by spacers that allow the regions of the peptides to be presented to the receptor in different ways. The distance between binding regions may be as little as 1 residue, or at least 2-20 residues, or up to at least 100 residues. Preferred spacers are 3, 6, 9, 12, 15, or 18 residues in length. For probing large binding sites or tandem binding sites (e.g., Site 1 and Site 2 of IR), the binding regions may be separated by a spacer of residues of up to 20 to 30 amino acids. The number of spacer residues when present will typically be at least 2 residues, and often will be less than 20 residues.

The oligonucleotide library may have binding sequences which are separated by spacers (e.g., linkers), and thus may be represented by the formula: $(NNK)_y - (abc)_n - (NNK)_z$ where N and K are as defined previously (note that S as defined previously may be substituted for K), and $y+z$ is equal to about 5, 6, 7, 8, or more, a, b and c represent the same or different nucleotides comprising a codon encoding spacer amino acids, n is up to about 3, 6, 9, or 12 amino acids, or more. The spacer residues may be somewhat flexible, comprising oligo-glycine, or oligo-glycine-glycine-serine, for example, to provide the diversity domains of the library with the ability to interact with sites in a large binding site relatively unconstrained by attachment to the phage protein. Rigid spacers, such as, e.g., oligo-proline, may also be inserted separately or in combination with other spacers, including glycine spacers. It may be desired to have the IR or IGF-1R binding sequences close to one another and use a spacer to orient the binding sequences with respect to each other, such as by employing a turn between the two sequences, as might be provided by a spacer of the

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sequence glycine-proline-glycine, for example. To add stability to such a turn, it may be desirable or necessary to add cysteine residues at either or both ends of each variable region. The cysteine residues would then form disulfide bridges to hold the variable regions together in a loop, and in this
5 fashion may also serve to mimic a cyclic peptide. Of course, those skilled in the art will appreciate that various other types of covalent linkages for cyclization may also be used.

Spacer residues as described above may also be situated on either or both ends of the IR or IGF-1R binding sequences. For instance, a cyclic
10 peptide may be designed without an intervening spacer, by having a cysteine residue on both ends of the peptide. As described above, flexible spacers, e.g., oligo-glycine, may facilitate interaction of the peptide with the selected receptors. Alternatively, rigid spacers may allow the peptide to be presented as if on the end of a rigid arm, where the number of residues,
15 e.g., proline residues, determines not only the length of the arm but also the direction for the arm in which the peptide is oriented. Hydrophilic spacers, made up of charged and/or uncharged hydrophilic amino acids, (e.g., Thr, His, Asn, Gln, Arg, Glu, Asp, Met, Lys, etc.), or hydrophobic spacers of hydrophobic amino acids (e.g., Phe, Leu, Ile, Gly, Val, Ala, etc.) may be
20 used to present the peptides to receptor binding sites with a variety of local environments.

Notably, some peptides, because of their size and/or sequence, may cause severe defects in the infectivity of their carrier phage. This causes a loss of phage from the population during reinfection and amplification
25 following each cycle of panning. To minimize problems associated with defective infectivity, DNA prepared from the eluted phage can be transformed into appropriate host cells, such as, e.g., *E. coli*, preferably by electroporation (see, e.g., Dower *et al.*, *Nucl. Acids Res.* **16**:6127-6145), or well known chemical means. The cells are cultivated for a period of time
30 sufficient for marker expression, and selection is applied as typically done for DNA transformation. The colonies are amplified, and phage harvested

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for affinity enrichment in accordance with established methods. Phage identified in the affinity enrichment may be re-amplified by infection into the host cells. The successful transformants are selected by growth in an appropriate antibiotic(s), e.g., tetracycline or ampicillin. This may be done
5 on solid or in liquid growth medium.

For growth on solid medium, the cells are grown at a high density (about 10^8 to 10^9 transformants per m^2) on a large surface of, for example, L-agar containing the selective antibiotic to form essentially a confluent lawn. The cells and extruded phage are scraped from the surface and
10 phage are prepared for the first round of panning (see, e.g., Parmley and Smith, 1988, *Gene* 73:305-318). For growth in liquid culture, cells may be grown in L-broth and antibiotic through about 10 or more doublings. The phage are harvested by standard procedures (see Sambrook *et al.*, 1989, *Molecular Cloning*, 2nd ed.). Growth in liquid culture may be more
15 convenient because of the size of the libraries, while growth on solid media likely provides less chance of bias during the amplification process.

For affinity enrichment of desired clones, generally about 10^3 to 10^4 library equivalents (a library equivalent is one of each recombinant; 10^4 equivalents of a library of 10^9 members is $10^9 \times 10^4 = 10^{13}$ phage), but
20 typically at least 10^2 library equivalents, up to about 10^5 to 10^6 , are incubated with a receptor (or portion thereof) to which the desired peptide is sought. The receptor is in one of several forms appropriate for affinity enrichment schemes. In one example the receptor is immobilized on a surface or particle, and the library of phage bearing peptides is then panned
25 on the immobilized receptor generally according to procedures known in the art. In an alternate scheme, a receptor is attached to a recognizable ligand (which may be attached via a tether). A specific example of such a ligand is biotin. The receptor, so modified, is incubated with the library of phage and binding occurs with both reactants in solution. The resulting complexes are
30 then bound to streptavidin (or avidin) through the biotin moiety. The streptavidin may be immobilized on a surface such as a plastic plate or on

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particles, in which case the complexes (phage/peptide/receptor/biotin/streptavidin) are physically retained; or the streptavidin may be labeled, with a fluorophor, for example, to tag the active phage/peptide for detection and/or isolation by sorting procedures, e.g., on a
5 fluorescence-activated cell sorter.

Phage that associate with IR or IGF-1R via non-specific interactions are removed by washing. The degree and stringency of washing required will be determined for each receptor/peptide of interest. A certain degree of control can be exerted over the binding characteristics of the peptides
10 recovered by adjusting the conditions of the binding incubation and the subsequent washing. The temperature, pH, ionic strength, divalent cation concentration, and the volume and duration of the washing will select for peptides within particular ranges of affinity for the receptor. Selection based on slow dissociation rate, which is usually predictive of high affinity, is the
15 most practical route. This may be done either by continued incubation in the presence of a saturating amount of free ligand, or by increasing the volume, number, and length of the washes. In each case, the rebinding of dissociated peptide-phage is prevented, and with increasing time, peptide-phage of higher and higher affinity are recovered. Additional modifications
20 of the binding and washing procedures may be applied to find peptides that bind receptors under special conditions. Once a peptide sequence that imparts some affinity and specificity for the receptor molecule is known, the diversity around this binding motif may be embellished. For instance, variable peptide regions may be placed on one or both ends of the identified
25 sequence. The known sequence may be identified from the literature, or may be derived from early rounds of panning in the context of the present invention.

G. Screening Assays

In another embodiment of this invention, screening assays to identify
30 pharmacologically active ligands at IR and/or IGF-1R are provided. Ligands

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may encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 daltons. Such ligands can comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. Ligands often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Ligands can also comprise biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof.

Ligands may include, for example, 1) peptides such as soluble peptides, including Ig-tailed fusion peptides and members of random peptide libraries (see, e.g., Lam *et al.*, 1991, *Nature* **354**:82-84; Houghten *et al.*, 1991, *Nature* **354**:84-86) and combinatorial chemistry-derived molecular libraries made of D- and/or L-configuration amino acids; 2) phosphopeptides (e.g., members of random and partially degenerate, directed phosphopeptide libraries, see, e.g., Songyang *et al.*, 1993, *Cell* **72**:767-778); 3) antibodies (e.g., polyclonal, monoclonal, humanized, anti-idiotypic, chimeric, and single chain antibodies as well as Fab, F(ab')₂, Fab expression library fragments, and epitope-binding fragments of antibodies); and 4) small organic and inorganic molecules.

Ligands can be obtained from a wide variety of sources including libraries of synthetic or natural compounds. Synthetic compound libraries are commercially available from, for example, Maybridge Chemical Co. (Trevillet, Cornwall, UK), Comgenex (Princeton, NJ), Brandon Associates (Merrimack, NH), and Microsource (New Milford, CT). A rare chemical library is available from Aldrich Chemical Company, Inc. (Milwaukee, WI). Natural compound libraries comprising bacterial, fungal, plant or animal extracts are available from, for example, Pan Laboratories (Bothell, WA). In

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addition, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides.

Alternatively, libraries of natural compounds in the form of bacterial,
5 fungal, plant and animal extracts can be readily produced. Methods for the synthesis of molecular libraries are readily available (see, e.g., DeWitt *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**:6909; Erb *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**:11422; Zuckermann *et al.*, 1994, *J. Med. Chem.* **37**:2678; Cho *et al.*, 1993, *Science* **261**:1303; Carell *et al.*, 1994, *Angew. Chem. Int. Ed. Engl.* **33**:2059; Carell *et al.*, 1994, *Angew. Chem. Int. Ed. Engl.* **33**:2061; and
10 in Gallop *et al.*, 1994, *J. Med. Chem.* **37**:1233). In addition, natural or synthetic compound libraries and compounds can be readily modified through conventional chemical, physical and biochemical means (see, e.g., Blondelle *et al.*, 1996, *Trends in Biotech.* **14**:60), and may be used to
15 produce combinatorial libraries. In another approach, previously identified pharmacological agents can be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, and the analogs can be screened for IR-modulating activity.

Numerous methods for producing combinatorial libraries are known in
20 the art, including those involving biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide or peptide libraries, while
25 the other four approaches are applicable to polypeptide, peptide, non-peptide oligomer, or small molecule libraries of compounds (K. S. Lam, 1997, *Anticancer Drug Des.* **12**:145).

Libraries may be screened in solution by methods generally known in the art for determining whether ligands competitively bind at a common
30 binding site. Such methods may including screening libraries in solution (e.g., Houghten, 1992, *Biotechniques* **13**:412-421), or on beads (Lam, 1991,

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Nature **354**:82-84), chips (Fodor, 1993, *Nature* **364**:555-556), bacteria or spores (Ladner U.S. Pat. No. 5,223,409), plasmids (Cull *et al.*, 1992, *Proc. Natl. Acad. Sci. USA* **89**:1865-1869), or on phage (Scott and Smith, 1990, *Science* **249**:386-390; Devlin, 1990, *Science* **249**:404-406; Cwirla *et al.*,
5 1990, *Proc. Natl. Acad. Sci. USA* **97**:6378-6382; Felici, 1991, *J. Mol. Biol.* **222**:301-310; Ladner, *supra*).

Where the screening assay is a binding assay, IR, or one of the IR-binding peptides disclosed herein, may be joined to a label, where the label can directly or indirectly provide a detectable signal. Various labels include
10 radioisotopes, fluorescent molecules, chemiluminescent molecules, enzymes, specific binding molecules, particles, e.g., magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin, etc. For the specific binding members, the complementary member would normally be labeled with a molecule that
15 provides for detection, in accordance with known procedures.

A variety of other reagents may be included in the screening assay. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Reagents that improve the
20 efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The components are added in any order that produces the requisite binding. Incubations are performed at any temperature that facilitates optimal activity, typically between 4° and 40°C. Incubation periods are selected for optimum activity, but may also be
25 optimized to facilitate rapid high-throughput screening. Normally, between 0.1 and 1 hr will be sufficient. In general, a plurality of assay mixtures is run in parallel with different test agent concentrations to obtain a differential response to these concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of
30 detection.

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The screening assays provided in accordance with this invention are based on those disclosed in International application WO 96/04557, which is incorporated herein in its entirety. Briefly, WO 96/04557 discloses the use of reporter peptides that bind to active sites on targets and possess agonist or antagonist activity at the target. These reporters are identified from recombinant libraries and are either peptides with random amino acid sequences or variable antibody regions with at least one CDR region that has been randomized (rVab). The reporter peptides may be expressed in cell recombinant expression systems, such as for example in *E. coli*, or by phage display (see WO 96/04557 and Kay *et al.* 1996, *Mol. Divers.* 1(2):139-40, both of which are incorporated herein by reference). The reporters identified from the libraries may then be used in accordance with this invention either as therapeutics themselves, or in competition binding assays to screen for other molecules, preferably small, active molecules, which possess similar properties to the reporters and may be developed as drug candidates to provide agonist or antagonist activity. Preferably, these small organic molecules are orally active.

The basic format of an *in vitro* competitive receptor binding assay as the basis of a heterogeneous screen for small organic molecular replacements for insulin may be as follows: occupation of the active site of IR is quantified by time-resolved fluorometric detection (TRFD) with streptavidin-labeled europium (saEu) complexed to biotinylated peptides (bP). In this assay, saEu forms a ternary complex with bP and IR (i.e., IR:bP:saEu complex). The TRFD assay format is well established, sensitive, and quantitative (Tompkins *et al.*, 1993, *J. Immunol. Methods* **163**:209-216). The assay can use a single-chain antibody or a biotinylated peptide. Furthermore, both assay formats faithfully report the competition of the biotinylated ligands binding to the active site of IR by insulin.

In these assays, soluble IR is coated on the surface of microtiter wells, blocked by a solution of 0.5% bovine serum albumin (BSA) and 2% non-fat milk in PBS, and then incubated with biotinylated peptide or rVab.

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Unbound bP is then washed away and saEu is added to complex with receptor-bound bP. Upon addition of the acidic enhancement solution, the bound europium is released as free Eu^{3+} which rapidly forms a highly fluorescent and stable complex with components of the enhancement solution. The IR:bP bound saEu is then converted into its highly fluorescent state and detected by a detector such as Wallac Victor II (EG&G Wallac, Inc.)

Phage display libraries can also be screened for ligands that bind to IR or IGF-1R, as described above. Details of the construction and analyses of these libraries, as well as the basic procedures for biopanning and selection of binders, have been published (see, e.g., WO 96/04557; Mandecki *et al.*, 1997, *Display Technologies – Novel Targets and Strategies*, P. Guttry (ed), International Business Communications, Inc. Southborough, MA, pp. 231-254; Ravera *et al.*, 1998, *Oncogene* **16**:1993-1999; Scott and Smith, 1990, *Science* **249**:386-390); Grihalde *et al.*, 1995, *Gene* **166**:187-195; Chen *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* **93**:1997-2001; Kay *et al.*, 1993, *Gene* **128**:59-65; Carcamo *et al.*, 1998, *Proc. Natl. Acad. Sci. USA* **95**:11146-11151; Hoogenboom, 1997, *Trends Biotechnol.* **15**:62-70; Rader and Barbas, 1997, *Curr. Opin. Biotechnol.* **8**:503-508; all of which are incorporated herein by reference).

The designing of mimetics to a known pharmaceutically active compound is a known approach to the development of pharmaceuticals based on a "lead" compound. This might be desirable where the active compound is difficult or expensive to synthesize or where it is unsuitable for a particular method of administration, e.g., peptides are generally unsuitable active agents for oral compositions as they tend to be quickly degraded by proteases in the alimentary canal. Mimetic design, synthesis, and testing are generally used to avoid large-scale screening of molecules for a target property.

There are several steps commonly taken in the design of a mimetic from a compound having a given target property. First, the particular parts

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of the compound that are critical and/or important in determining the target property are determined. In the case of a peptide, this can be done by systematically varying the amino acid residues in the peptide (e.g., by substituting each residue in turn). These parts or residues constituting the
5 active region of the compound are known as its "pharmacophore".

Once the pharmacophore has been found, its structure is modeled according to its physical properties (e.g., stereochemistry, bonding, size, and/or charge), using data from a range of sources (e.g., spectroscopic techniques, X-ray diffraction data, and NMR). Computational analysis,
10 similarity mapping (which models the charge and/or volume of a pharmacophore, rather than the bonding between atoms), and other techniques can be used in this modeling process.

In a variant of this approach, the three dimensional structure of the ligand and its binding partner are modeled. This can be especially useful
15 where the ligand and/or binding partner change conformation on binding, allowing the model to take account of this in the design of the mimetic.

A template molecule is then selected, and chemical groups that mimic the pharmacophore can be grafted onto the template. The template molecule and the chemical groups grafted on to it can conveniently be
20 selected so that the mimetic is easy to synthesize, is likely to be pharmacologically acceptable, does not degrade *in vivo*, and retains the biological activity of the lead compound. The mimetics found are then screened to ascertain the extent they exhibit the target property, or to what extent they inhibit it. Further optimization or modification can then be carried
25 out to arrive at one or more final mimetics for *in vivo* or clinical testing.

This invention provides specific IR and IGF-1R amino acid sequences that function as either agonists or antagonists at IR and/or IGF-1R. Additional sequences may be obtained in accordance with the procedures described herein.

H. Use of the Peptides Provided by this Invention

The IR and IGF-1R agonist and antagonist peptides provided by this invention are useful as lead compounds for identifying other more potent or selective therapeutics, assay reagents for identifying other useful ligands by, for example, competition screening assays, as research tools for further analysis of IR and IGF-1R, and as potential therapeutics in pharmaceutical compositions. In one embodiment, one or more of the disclosed peptides can be provided as components in a kit for identifying other ligands (e.g., small, organic molecules) that bind to IR or IGF-1R. Such kits may also comprise IR or IGF-1R, or functional fragments thereof. The peptide and receptor components of the kit may be labeled (e.g., by radioisotopes, fluorescent molecules, chemiluminescent molecules, enzymes or other labels), or may be unlabeled and labeling reagents may be provided. The kits may also contain peripheral reagents such as buffers, stabilizers, etc. Instructions for use can also be provided.

In another embodiment, the peptide sequences provided by this invention can be used to design secondary peptide libraries, which are derived from the peptide sequences, and include members that bind to Site 1 and/or Site 2 of IR or IGF-1R. Such libraries can be used to identify sequence variants that increase or modulate the binding and/or activity of the original peptide at IR or IGF-1R, as described in the related applications of Beasley *et al.* International Application PCT/US00/08528, filed March 29, 2000, and Beasley *et al.*, U.S. Application Serial No. 09/538,038, filed March 29, 2000, in accordance with well-established techniques.

IR agonist amino acid sequences provided by this invention are useful as insulin analogs and may therefore be developed as treatments for diabetes or other diseases associated with a decreased response or production of insulin. For use as an insulin supplement or replacement, non-limiting examples of amino acid sequences include D117/H2C: FHENFYDWFVRQVSK (SEQ ID NO:1780); D117/H2C minus terminal lysine: FHENFYDWFVRQVS (SEQ ID NO:1557); D118:

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DYKDFYDAIQLVRSARAGGTRDKK (SEQ ID NO:1781); D118 minus
FLAG® tag and terminal lysines: FYDAIQLVRSARAGGTRD (SEQ ID
NO:1782); D119: KDRAFYNGLRDLVGAVYGAWDKK (SEQ ID NO:1733);
D119 minus terminal lysines: KDRAFYNGLRDLVGAVYGAWD (residues 1-
5 21 of SEQ ID NO: 1733); D116/JBA5: DYKDLQCQSWGVRIGWLAGLCPKK
(SEQ ID NO:1541); D116/JBA5 minus FLAG® tag and terminal lysines:
LCQSWGVRIGWLAGLCP (SEQ ID NO:1542); D113/H2:
DYKDVTFTSAVFHENFYDWFVRQVSKK (SEQ ID NO:1783); D113/H2
minus FLAG® tag and terminal lysines: VTFTSAVFHENFYDWFVRQVS
10 (SEQ ID NO:1784); and S175: GRVDWLQRNANFYDWFVAELG (SEQ ID
NO:1560). Preferred peptide dimer sequences are represented by S325,
S332, S333, S335, S337, S353, S374-S376, S378, S379, S381, S414,
S415, and S418 (see Table 7). Other preferred dimers sequences are
represented by S455, S457, S458, S467, S468, S471, S499, S510, S518,
15 S519, and S520 sequences (see Table 7). Especially preferred is the S519
dimer sequence, which shows *in vitro* and *in vivo* activity comparable to
insulin (see Figures 31A-C, 32A-B, and 33), S557 (see, e.g., Figure 55), and
S597 (see, e.g., Figures 54-56).

IGF-1R antagonist amino acid sequences provided by this invention
20 are useful as treatments for cancers, including, but not limited to, breast,
prostate, colorectal, and ovarian cancers. Human and breast cancers are
responsible for over 40,000 deaths per year, as present treatments such as
surgery, chemotherapy, radiation therapy, and immunotherapy show limited
success. The IGF-1R antagonist amino acid sequences disclosed herein
25 are also useful for the treatment or prevention of diabetic retinopathy.
Recent reports have shown that a previously identified IGF-1R antagonist
can suppress retinal neovascularization, which causes diabetic retinopathy
(Smith *et al.*, 1999, *Nat. Med.* 5:1390-1395).

IGF-1R agonist amino acid sequences provided by this invention are
30 useful for development as treatments for neurological disorders, including
stroke and diabetic neuropathy. Reports of several different groups

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implicate IGF-1R in the reduction of global brain ischemia, and support the use of IGF-1 for the treatment of diabetic neuropathy (reviewed in Auer *et al.*, 1998, *Neurology* **51**:S39-S43; Apfel, 1999, *Am. J. Med.* **107**:34S-42S).

I. Modification of Peptides

5 The peptides of the invention may be subjected to one or more modifications known in the art, which may be useful for manipulating storage stability, pharmacokinetics, and/or any aspect of the bioactivity of the peptide, such as, e.g., potency, selectivity, and drug interaction. Chemical modification to which the peptides may be subjected includes, without
10 limitation, the conjugation to a peptide of one or more of polyethylene glycol (PEG), monomethoxy-polyethylene glycol, dextran, poly-(N-vinyl pyrrolidone) polyethylene glycol, propylene glycol homopolymers, a polypropylene oxide/ethylene oxide co-polymer, polypropylene glycol, polyoxyethylated polyols (e.g., glycerol) and polyvinyl alcohol, colominic
15 acids or other carbohydrate based polymers, polymers of amino acids, and biotin derivatives. PEG conjugation of proteins at Cys residues is disclosed, e.g., in Goodson, R. J. & Katre, N. V. (1990) *Bio/Technology* **8**, 343 and Kogan, T. P. (1992) *Synthetic Comm.* **22**, 2417.

 Other useful modifications include, without limitation, acylation, using
20 methods and compositions such as described in, e.g., U.S. Patent Serial No. 6,251, 856, and WO 00/55119.

J. Therapeutic Administration

 The peptides of the present invention may be administered
25 individually or in combination with other pharmacologically active agents. It will be understood that such combination therapy encompasses different therapeutic regimens, including, without limitation, administration of multiple agents together in a single dosage form or in distinct, individual dosage forms. If the agents are present in different dosage forms, administration

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may be simultaneous or near-simultaneous or may follow any predetermined regimen that encompasses administration of the different agents.

For example, when used to treat diabetes or other diseases or syndromes associated with a decreased response or production of insulin, hyperlipidemia, obesity, appetite-related syndromes, and the like, the peptides of the invention may be advantageously administered in a combination treatment regimen with one or more agents, including, without limitation, insulin, insulin analogues, insulin derivatives, glucagon-like peptide-1 or-2 (GLP-1, GLP-2), derivatives or analogues of GLP-1 or GLP-2 (such as are disclosed, e.g., in WO 00/55119). It will be understood that an "analogue" of insulin, GLP-1, or GLP-2 as used herein refers to a peptide containing one or more amino acid substitutions relative to the native sequence of insulin, GLP-1, or GLP-2, as applicable; and "derivative" of insulin, GLP-1, or GLP-2 as used herein refers to a native or analogue insulin, GLP-1, or GLP-2 peptide that has undergone one or more additional chemical modifications of the amino acid sequence, in particular relative to the natural sequence. Insulin derivatives and analogues are disclosed, e.g., in U.S. Patent Serial No. 5,656,722, 5,750,497, 6,251,856, and 6,268,335.

In some embodiments, the combination agent is one of Lys^{B29}(-myristoyl)des(B30) human insulin, Lys^{B29}(-tetradecanoyl)des(B30) human insulin and B²⁹-N-(N-lithocolyl)-glutamyl-des(B30) human insulin. Also suitable for combination therapy are non-peptide antihyperglycemic agents, antihyperlipidemic agents, and the like such as those well-known in the art.

In one embodiment, the invention encompasses methods of treating diabetes or related syndromes comprising administering a first amount of peptide S597 or peptide S557 and a second amount of a long-acting insulin analogue, such as, e.g., Lys^{B29}(-myristoyl)des(B30) human insulin, Lys^{B29}(-tetradecanoyl)des(B30) human insulin. or B²⁹-N-(N-lithocolyl)-glutamyl-des(B30) human insulin, wherein the first and second amounts together are effective for treating the syndrome. As used herein, a long-

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acting insulin analogue is one that exhibits a protracted profile of action relative to native human insulin, as disclosed, e.g., in U.S. Patent Serial No. 6,451,970.

The peptides of the present invention may be administered
5 individually or in combination with other pharmacologically active agents. It will be understood that such combination therapy encompasses different therapeutic regimens, including, without limitation, administration of multiple agents together in a single dosage form or in distinct, individual dosage forms. If the agents are present in different dosage forms, administration
10 may be simultaneous or near-simultaneous or may follow any predetermined regimen that encompasses administration of the different agents.

For example, when used to treat diabetes or other diseases or syndromes associated with a decreased response or production of insulin,
15 hyperlipidemia, obesity, appetite-related syndromes, and the like, the peptides of the invention may be advantageously administered in a combination treatment regimen with one or more agents, including, without limitation, insulin, insulin analogues, insulin derivatives, glucagon-like peptide-1 or-2 (GLP-1, GLP-2), derivatives or analogues of GLP-1 or GLP-2
20 (such as are disclosed, e.g., in WO 00/55119). It will be understood that an "analogue" of insulin, GLP-1, or GLP-2 as used herein refers to a peptide containing one or more amino acid substitutions relative to the native sequence of insulin, GLP-1, or GLP-2, as applicable; and "derivative" of insulin, GLP-1, or GLP-2 as used herein refers to a native or analogue
25 insulin, GLP-1, or GLP-2 peptide that has undergone one or more additional chemical modifications of the amino acid sequence, in particular relative to the natural sequence. Insulin derivatives and analogues are disclosed, e.g., in U.S. Patent Serial No. 5,656,722, 5,750,497, 6,251,856, and 6,268,335. In some embodiments, the combination agent is one of Lys^{B29}(-
30 myristoyl)des(B30) human insulin, Lys^{B29}(-tetradecanoyl)des(B30) human insulin and B²⁹-N -(N-lithocolyl- -glutamyl)-des(B30) human insulin. Also

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suitable for combination therapy are non-peptide antihyperglycemic agents, antihyperlipidemic agents, and the like such as those well-known in the art.

In one embodiment, the invention encompasses methods of treating diabetes or related syndromes comprising administering a first amount of peptide S597 or peptide S557 and a second amount of a long-acting insulin analogue, such as, e.g., Lys^{B29}(-myristoyl)des(B30) human insulin, Lys^{B29}(-tetradecanoyl)des(B30) human insulin. or B²⁹-N-(N-lithocolyl-glutamyl)-des(B30) human insulin, wherein the first and second amounts together are effective for treating the syndrome. As used herein, a long-acting insulin analogue is one that exhibits a protracted profile of action relative to native human insulin, as disclosed, e.g., in U.S. Patent Serial No. 6,451,970.

K. Methods of Administration

The amino acid sequences of this invention may be administered as pharmaceutical compositions comprising standard carriers known in the art for delivering proteins and peptides and by gene therapy. Preferably, a pharmaceutical composition includes, in admixture, a pharmaceutically (i.e., physiologically) acceptable carrier, excipient, or diluent, and one or more of an IR or IGF-1R agonist or antagonist peptide, as an active ingredient. The preparation of pharmaceutical compositions that contain peptides as active ingredients is well understood in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions, however, solid forms suitable for solution in, or suspension in, liquid prior to injection can also be prepared. The preparation can also be emulsified. The active therapeutic ingredient is often mixed with excipients that are pharmaceutically (i.e., physiologically) acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the composition can contain minor amounts of auxiliary

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substances such as wetting or emulsifying agents, pH-buffering agents, which enhance the effectiveness of the active ingredient.

An IR or IGF-1R agonist or antagonist peptide can be formulated into a pharmaceutical composition as neutralized physiologically acceptable salt
5 forms. Suitable salts include the acid addition salts (i.e., formed with the free amino groups of the peptide molecule) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed from the free carboxyl groups can also be derived from inorganic
10 bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

The pharmaceutical compositions can be administered systemically by oral or parenteral routes. Non-limiting parenteral routes of administration
15 include subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation, intranasal, intra-arterial, intrathecal, enteral, sublingual, or rectal. Due to the labile nature of the amino acid sequences parenteral administration is preferred. Preferred modes of administration include aerosols for nasal or bronchial absorption; suspensions for
20 intravenous, intramuscular, intrasternal or subcutaneous, injection; and compounds for oral administration.

Intravenous administration, for example, can be performed by injection of a unit dose. The term "unit dose" when used in reference to a pharmaceutical composition of the present invention refers to physically
25 discrete units suitable as unitary dosage for humans, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent; i.e., liquid used to dilute a concentrated or pure substance (either liquid or solid), making that substance the correct (diluted) concentration for use. For injectable
30 administration, the composition is in sterile solution or suspension or may be emulsified in pharmaceutically- and physiologically-acceptable aqueous or

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oleaginous vehicles, which may contain preservatives, stabilizers, and material for rendering the solution or suspension isotonic with body fluids (i.e., blood) of the recipient.

Excipients suitable for use are water, phosphate buffered saline, pH
5 7.4, 0.15 M aqueous sodium chloride solution, dextrose, glycerol, dilute ethanol, and the like, and mixtures thereof. Illustrative stabilizers are polyethylene glycol, proteins, saccharides, amino acids, inorganic acids, and organic acids, which may be used either on their own or as admixtures. The amounts or quantities, as well as routes of administration, used are
10 determined on an individual basis, and correspond to the amounts used in similar types of applications or indications known to those of skill in the art.

Pharmaceutical compositions are administered in a manner compatible with the dosage formulation, and in a therapeutically effective amount. The quantity to be administered depends on the subject to be
15 treated, capacity of the subject's immune system to utilize the active ingredient, and degree of modulation of IR or IGF-1R activity desired. Precise amounts of active ingredient required to be administered depend on the judgment of the practitioner and are specific for each individual. However, suitable dosages may range from about 10 to 200 nmol active
20 peptide per kilogram body weight of individual per day and depend on the route of administration. Suitable regimes for initial administration and booster shots are also variable, but are typified by an initial administration followed by repeated doses at one or more hour intervals by a subsequent injection or other administration. Alternatively, continuous intravenous
25 infusions sufficient to maintain picomolar concentrations (e.g., approximately 1 pM to approximately 10 nM) in the blood are contemplated. An exemplary formulation comprises the IR or IGF-1R agonist or antagonist peptide in a mixture with sodium busulfite USP (3.2 mg/ml); disodium edetate USP (0.1 mg/ml); and water for injection q.s.a.d. (1 ml).

30 Further guidance in preparing pharmaceutical formulations can be found in, e.g., Gilman *et al.* (eds), 1990, *Goodman and Gilman's: The*

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Pharmacological Basis of Therapeutics, 8th ed., Pergamon Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis *et al.* (eds), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman *et al.* (eds), 1990,
5 *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

The present invention further contemplates compositions comprising an IR or IGF-1R agonist or antagonist peptide, and a physiologically acceptable carrier, excipient, or diluent as described in detail herein.

The constructs as described herein may also be used in gene
10 transfer and gene therapy methods to allow the expression of one or more amino acid sequences of the present invention. The amino acid sequences of the present invention can be used for gene therapy and thereby provide an alternative method of treating diabetes which does not rely on the administration or expression of insulin. Expressing insulin for use in gene
15 therapy requires the expression of a precursor product, which must then undergo processing including cleavage and disulfide bond formation to form the active product. The amino acid sequences of this invention, which possess activity, are relatively small, and thus do not require the complex processing steps to become active. Accordingly, these sequences provide a
20 more suitable product for gene therapy.

Gene transfer systems known in the art may be useful in the practice of the gene therapy methods of the present invention. These include viral and non-viral transfer methods. A number of viruses have been used as gene transfer vectors, including polyoma, *i.e.*, SV40 (Madzak *et al.*, 1992, *J. Gen. Virol.*, **73**:1533-1536), adenovirus (Berkner, 1992, *Curr. Top. Microbiol. Immunol.*, **158**:39-6; Berkner *et al.*, 1988, *Bio Techniques*, **6**:616-629; Gorziglia *et al.*, 1992, *J. Virol.*, **66**:4407-4412; Quantin *et al.*, 1992, *Proc. Natl. Acad. Sci. USA*, **89**:2581-2584; Rosenfeld *et al.*, 1992, *Cell*, **68**:143-155; Wilkinson *et al.*, 1992, *Nucl. Acids Res.*, **20**:2233-2239; Stratford-
25 Perricaudet *et al.*, 1990, *Hum. Gene Ther.*, **1**:241-256), vaccinia virus (Mackett *et al.*, 1992, *Biotechnology*, **24**:495- 499), adeno-associated virus

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(Muzyczka, 1992, *Curr. Top. Microbiol. Immunol.* **158**:91- 123; Ohi *et al.*, 1990, *Gene*, **89**:279-282), herpes viruses including HSV and EBV (Margolskee, 1992, *Curr. Top. Microbiol. Immunol.* **158**:67-90; Johnson *et al.*, 1992, *J. Virol.*, **66**:2952-2965; Fink *et al.*, 1992, *Hum. Gene Ther.* **3**:11-19; Breakfield *et al.*, 1987, *Mol. Neurobiol.*, **1**:337-371; Fresse *et al.*, 1990, *Biochem. Pharmacol.* **40**:2189-2199), and retroviruses of avian (Brandyopadhyay *et al.*, 1984, *Mol. Cell Biol.*, **4**:749-754; Petropoulos *et al.*, 1992, *J. Virol.*, **66**:3391-3397), murine (Miller, 1992, *Curr. Top. Microbiol. Immunol.* **158**:1-24; Miller *et al.*, 1985, *Mol. Cell Biol.*, **5**:431-437; Sorge *et al.*, 1984, *Mol. Cell Biol.*, **4**:1730-1737; Mann *et al.*, 1985, *J. Virol.*, **54**:401-407), and human origin (Page *et al.*, 1990, *J. Virol.*, **64**:5370-5276; Buchschalcher *et al.*, 1992, *J. Virol.*, **66**:2731-2739). Most human gene therapy protocols have been based on disabled murine retroviruses.

Non-viral gene transfer methods known in the art include chemical techniques such as calcium phosphate coprecipitation (Graham *et al.*, 1973, *Virology*, **52**:456-467; Pellicer *et al.*, 1980, *Science*, **209**:1414-1422), mechanical techniques, for example microinjection (Anderson *et al.*, 1980, *Proc. Natl. Acad. Sci. USA*, **77**:5399-5403; Gordon *et al.*, 1980, *Proc. Natl. Acad. Sci. USA*, **77**:7380-7384; Brinster *et al.*, 1981, *Cell*, **27**:223-231; Constantini *et al.*, 1981, *Nature*, **294**:92-94), membrane fusion-mediated transfer via liposomes (Felgner *et al.*, 1987, *Proc. Natl. Acad. Sci. USA*, **84**:7413-7417; Wang *et al.*, 1989, *Biochemistry*, **28**:9508-9514; Kaneda *et al.*, 1989, *J. Biol. Chem.*, **264**:12126-12129; Stewart *et al.*, 1992, *Hum. Gene Ther.* **3**:267-275; Nabel *et al.*, 1990, *Science*, **249**:1285-1288; Lim *et al.*, 1992, *Circulation*, **83**:2007-2011; U.S. Patent Nos. 5,283,185 and 5,795,587), and direct DNA uptake and receptor-mediated DNA transfer (Wolff *et al.*, 1990, *Science*, **247**:1465-1468; Wu *et al.*, 1991, *BioTechniques*, **11**:474-485; Zenke *et al.*, 1990, *Proc. Natl. Acad. Sci. USA*, **87**:3655-3659; Wu *et al.*, 1989, *J. Biol. Chem.*, **264**:16985-16987; Wolff *et al.*, 1991, *BioTechniques*, **11**:474-485; Wagner *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, **88**:4255-4259; Cotten *et al.*,

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1990, *Proc. Natl. Acad. Sci. USA*, **87**:4033-4037; Curiel *et al.*, 1991, *Proc. Natl. Acad. Sci. USA*, **88**:8850-8854; Curiel *et al.*, 1991, *Hum. Gene Ther.* **3**:147-154).

Many types of cells and cell lines (e.g., primary cell lines or
5 established cell lines) and tissues are capable of being stably transfected
by or receiving the constructs of the invention. Examples of cells that
may be used include, but are not limited to, stem cells, B lymphocytes, T
lymphocytes, macrophages, other white blood lymphocytes (e.g.,
myelocytes, macrophages, or monocytes), immune system cells of
10 different developmental stages, erythroid lineage cells, pancreatic cells,
lung cells, muscle cells, liver cells, fat cells, neuronal cells, glial cells,
other brain cells, transformed cells of various cell lineages corresponding
to normal cell counterparts (e.g., K562, HEL, HL60, and MEL cells), and
established or otherwise transformed cells lines derived from all of the
15 foregoing. In addition, the constructs of the present invention may be
transferred by various means directly into tissues, where they would
stably integrate into the cells comprising the tissues. Further, the
constructs containing the DNA sequences of the peptides of the invention
can be introduced into primary cells at various stages of development,
20 including the embryonic and fetal stages, so as to effect gene therapy at
early stages of development.

In one approach, plasmid DNA is complexed with a polylysine-
conjugated antibody specific to the adenovirus hexon protein, and the
resulting complex is bound to an adenovirus vector. The trimolecular
25 complex is then used to infect cells. The adenovirus vector permits
efficient binding, internalization, and degradation of the endosome before
the coupled DNA is damaged.

In another approach, liposome/DNA is used to mediate direct *in vivo*
gene transfer. While in standard liposome preparations the gene transfer
30 process is non-specific, localized *in vivo* uptake and expression have been

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reported in tumor deposits, for example, following direct *in situ* administration (Nabel, 1992, *Hum. Gene Ther.* **3**:399-410).

Suitable gene transfer vectors possess a promoter sequence, preferably a promoter that is cell-specific and placed upstream of the sequence to be expressed. The vectors may also contain, optionally, one or more expressible marker genes for expression as an indication of successful transfection and expression of the nucleic acid sequences contained in the vector. In addition, vectors can be optimized to minimize undesired immunogenicity and maximize long-term expression of the desired gene product(s) (see Nabe, 1999, *Proc. Natl. Acad. Sci. USA* **96**:324-326). Moreover, vectors can be chosen based on cell-type that is targeted for treatment.

Illustrative examples of vehicles or vector constructs for transfection or infection of the host cells include replication-defective viral vectors, DNA virus or RNA virus (retrovirus) vectors, such as adenovirus, herpes simplex virus and adeno-associated viral vectors. Adeno-associated virus vectors are single stranded and allow the efficient delivery of multiple copies of nucleic acid to the cell's nucleus. Preferred are adenovirus vectors. The vectors will normally be substantially free of any prokaryotic DNA and may comprise a number of different functional nucleic acid sequences. An example of such functional sequences may be a DNA region comprising transcriptional and translational initiation and termination regulatory sequences, including promoters (e.g., strong promoters, inducible promoters, and the like) and enhancers which are active in the host cells. Also included as part of the functional sequences is an open reading frame (polynucleotide sequence) encoding a protein of interest. Flanking sequences may also be included for site-directed integration. In some situations, the 5'-flanking sequence will allow homologous recombination, thus changing the nature of the transcriptional initiation region, so as to provide for inducible or non-inducible transcription to increase or decrease the level of transcription, as an example.

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In general, the encoded and expressed peptide may be intracellular, i.e., retained in the cytoplasm, nucleus, or in an organelle, or may be secreted by the cell. For secretion, a signal sequence may be fused to the peptide sequence. As previously mentioned, a marker may be present for
5 selection of cells containing the vector construct. The marker may be an inducible or non-inducible gene and will generally allow for positive selection under induction, or without induction, respectively. Examples of marker genes include neomycin, dihydrofolate reductase, glutamine synthetase, and the like. The vector employed will generally also include an origin of
10 replication and other genes that are necessary for replication in the host cells, as routinely employed by those having skill in the art. As an example, the replication system comprising the origin of replication and any proteins associated with replication encoded by a particular virus may be included as part of the construct. The replication system must be selected so that the
15 genes encoding products necessary for replication do not ultimately transform the cells. Such replication systems are represented by replication-defective adenovirus (see G. Acsadi *et al.*, 1994, *Hum. Mol. Genet.* 3:579-584) and by Epstein-Barr virus. Examples of replication defective vectors, particularly, retroviral vectors that are replication
20 defective, are BAG, (see Price *et al.*, 1987, *Proc. Natl. Acad. Sci. USA*, 84:156; Sanes *et al.*, 1986, *EMBO J.*, 5:3133). It will be understood that the final gene construct may contain one or more genes of interest, for example, a gene encoding a bioactive metabolic molecule. In addition, cDNA, synthetically produced DNA or chromosomal DNA may be employed
25 utilizing methods and protocols known and practiced by those having skill in the art.

According to one approach for gene therapy, a vector encoding an IR or IGF-1R agonist or antagonist peptide is directly injected into the recipient cells (*in vivo* gene therapy). Alternatively, cells from the intended recipients
30 are explanted, genetically modified to encode an IR or IGF-1R agonist or antagonist peptide, and reimplanted into the donor (*ex vivo* gene therapy).

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An *ex vivo* approach provides the advantage of efficient viral gene transfer, which is superior to *in vivo* gene transfer approaches. In accordance with *ex vivo* gene therapy, the host cells are first transfected with engineered vectors containing at least one gene encoding an IR or IGF-1R agonist or antagonist peptide, suspended in a physiologically acceptable carrier or excipient such as saline or phosphate buffered saline, and the like, and then administered to the host or host cells. The desired gene product is expressed by the injected cells, which thus introduce the gene product into the host. The introduced gene products can thereby be utilized to treat or ameliorate a disorder that is related to altered insulin or IGF-1 levels (e.g., diabetes).

The described constructs may be administered in the form of a pharmaceutical preparation or composition containing a pharmaceutically acceptable carrier and a physiological excipient, in which preparation the vector may be a viral vector construct, or the like, to target the cells, tissues, or organs of the recipient organism of interest, including human and non-human mammals. The composition may be formed by dispersing the components in a suitable pharmaceutically acceptable liquid or solution such as sterile physiological saline or other injectable aqueous liquids. The amounts of the components to be used in such compositions may be routinely determined by those having skill in the art. The compositions may be administered by parenteral routes of injection, including subcutaneous, intravenous, intramuscular, and intrasternal.

EXAMPLES

The examples as set forth herein are meant to exemplify the various aspects of the present invention and are not intended to limit the invention in any way.

The following materials were used in the examples described below. Soluble IGF-1R was obtained from R&D Systems (Minneapolis, MN; Cat. # 391-GR/CF). Insulin receptor was prepared according to Bass *et al.*, 1996.

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The insulin was either from Sigma (St. Louis, MO; Cat. # I-0259) or Boehringer. The IGF-1 was from PeproTech (Cat. # 100-11). All synthetic peptides were synthesized by Novo Nordisk, AnaSpec, Inc. (San Jose, CA), PeptioGenics (Livermore, CA), or Research Genetics (Huntsville, AL) at
5 >80% purity. The Maxisorb Plates were from NUNC via Fisher (Cat. # 12565347). The HRP/Anti-M13 conjugate was from Pharmacia (Cat. # 27-9421-01). The ABTS solution was from BioF/X (Cat. # ABTS-0100-04).

Example 1: Monomer and Dimer Peptides

A. Cloning

10 Monomer and dimer peptides were constructed and expressed as protein fusions to a chitin binding domain (CBD) using the pTYB2 vector from the IMPACT™-CN system (New England Biolabs (NEB), Beverly, MA). The pTYB2 vector encodes a protein-splicing element (termed intein), which initiates self-cleavage upon the addition of DTT. The intein self-cleavage
15 separates the dimer from the affinity tag, to allow purification.

In the pTYB2 construct, the C-terminus of the peptide sequence was fused to the N-terminus of the intein/CBD sequence. Two peptide-flanking epitope tags were included: a shortened-FLAG® at the N-terminus and E-Tag at the C-terminus. This fusion was generated by ligating a vector
20 fragment encoding the intein/CBD with a PCR product encoding the peptide of interest.

The vector fragment was obtained by digesting at appropriate restriction sites the pTBY2 vector. The digested DNA fragment was resolved on a 1% agarose gel, excised, and purified by QIAEXII (QIAGEN,
25 Valencia, CA). To obtain the PCR product of the target proteins, primers were synthesized which anneal to appropriate sequences. The vector and insert were ligated overnight at 15°C. The ligation product was purified using QIAquick spin columns (QIAGEN) and electroporations were

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performed at 1500 V in an electroporation cuvette (0.1 mm gap; 0.5 ml volume) containing 10 ng of DNA and 40 μ l of *E. coli* strain BL21.

Immediately following electroporation, 1 ml of pre-warmed (40°C) 2xYT medium containing 2% glucose (2xYT-G) was added to the
5 transformants. The transformants were grown at 37°C for 1 h, and then plated onto 2xYT-AG plates and incubated overnight at 37°C. Individual colonies were isolated and used to inoculate 2xYT-G. The cultures were grown overnight at 37°C. Plasmid DNA was isolated from the cultures and sequencing was performed to confirm that the correct construct was
10 obtained.

B. Small-scale expression of peptide-CBD fusion proteins

E. coli ER2566 (New England Biolabs) containing plasmids encoding peptide-CBD fusion proteins were grown in 2xYT-AG at 37°C overnight, with agitation (250 rpm). The following day, the cultures were used to inoculate
15 media (2x YT-G) to obtain an OD₆₀₀ of 0.1. Upon reaching an OD₆₀₀ of 0.6, expression of the fusion protein was induced by the addition of IPTG (isopropyl- β -D-thiogalactopyranoside) to a final concentration of 0.3 mM. Cells were grown for 3 h. Following this, cells were pelleted by centrifugation and the cell pellets were analyzed by SDS-PAGE
20 electrophoresis. Production of the correct molecular weight fusion proteins was confirmed by Western blot analysis using the monoclonal antibody anti-E-Tag-HRP conjugate (Amersham Pharmacia).

C. Large-scale expression and purification of soluble peptide-CBD fusion proteins

E. coli ER2566 carrying plasmids encoding the fusion proteins were grown in 2xYT-AG media at 37°C for 8 h, with agitation (250 rpm). The cultures were back-diluted into to 2 L volumes of 2xYT-A to achieve an OD₆₀₀ of 0.1. Upon reaching an OD₆₀₀ of 0.5, IPTG was added to a final concentration of 0.3 mM. Cells were grown at 30°C overnight. The next day
30 cells were isolated by centrifugation. Samples of the cell pellet were

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analyzed by SDS-PAGE followed by the Western blot analysis using the mouse monoclonal antibody anti-E-Tag-HRP conjugate (Pharmacia) to visualize the expressed product.

D. Purification

5 The cell pellets were disrupted mechanically by sonication or chemically by treatment with the mild detergent. After removal of cell debris by centrifugation, the soluble proteins in the clarified lysate were prepared for chromatographic purification by dilution or dialysis into the appropriate starting buffer. The CBD fusions were purified by chitin affinity
10 chromatography according to the manufacturer's instructions (New England Biolabs). The lysate was loaded onto a chitin affinity column and the column was washed with 10 volumes of column buffer. Three bed volumes of the DTT containing cleavage buffer were loaded onto the column and the column was incubated overnight. The next day, the target protein was
15 eluted by continuing the flow of the cleavage buffer without DTT. The purified proteins were analyzed for purity and integrity by SDS-PAGE and Western blot analysis according to standard protocols.

Example 2: PEG-Based Dimer Peptides

A. Synthesis of the aldehyde containing peptide

20 The peptide was synthesized by stepwise solid phase synthesis on Rink amide Tentagel (0.21 mmol/g). Three equivalents of Fmoc-amino acids were used. The serine residue was introduced into the peptide by either coupling Fmoc-Ser(tBu)-OH to the N-terminal peptide or coupling Boc-Ser(tBu) to a selectively protected lysine side-chain. The peptide was
25 then deprotected and cleaved from the resin by treatment with 95% TFA (trifluoroacetic acid; aq) containing TIS (triisopropylsilan). Periodate oxidation, using 2 equivalent of NaIO₄ in 20% DMSO (dimethyl sulfoxide)-80% phosphate buffer pH 7.5 (45 µl/µmol peptide) for 5 min at room

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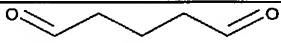

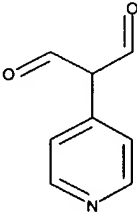
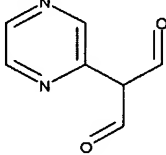
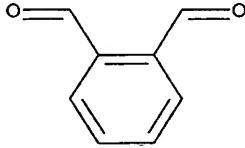
temperature (RT), converted the 2-amino alcohol moiety in an α -oxoacyl group. The peptide was purified immediately following oxidation.

B. Synthesis of the PEG-based dimer

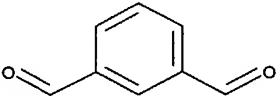

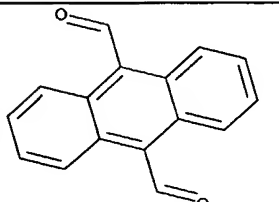
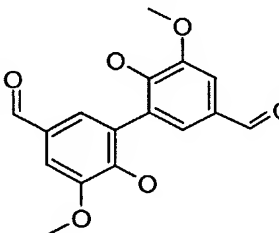


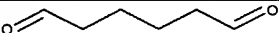
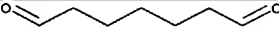

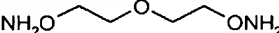
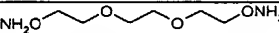
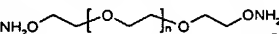
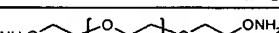
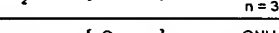
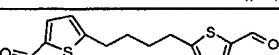
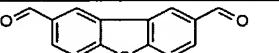
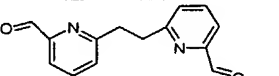
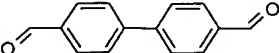
The unprotected and oxidized peptide (4.2 equivalent) was dimerized
 5 on the dioxyamino-PEG (polyethylene glycol)-linker (1 equivalent) in 90% DMSO-10% 20 mM NaOAc buffer, pH 5.1 (4.2 μ l/ μ mol peptide). The solution was left for 1 hr at 38°C and the progress of the reaction was monitored by MALDI-MS (matrix-assisted laser desorption/ionization mass spectrometry). Following this, the crude dimer was purified by semi-
 10 preparative HPLC (high performance liquid chromatography).

The molecular weights and inter peptide distance of various linkers is shown in Table 3, below.

TABLE 3

Structure	Number	MW	MW (- 2H ₂ O)
	1	100.1	64.1
	2	58.04	22.04
	3	149.15	113.15
	4	150.14	114.14
	5	134.13	98.13

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	6	134.13	98.13
	7	134.13	98.13
	8	234.25	198.25
	9	302.3	266.3
	10	72.06	36.06
	11	86.09	50.09
	12	114.14	78.14
	13	128.08	92.08
	14	142.19	106.19
(HCO)₄-(Lys)₂-Lys-Gly-NH₂	15		
	16	136.2	100.2
	17	180.2	144.2
	18	224.3	188.3
	19	268.3	232.3
	20	312.4	276.4
	21	278.4	242.4
	22	240.3	204.3
	23	240.3	204.3
	24	210.2	192.2

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Example 3: Determination of Insulin Receptor Binding

IR was incubated with ^{125}I -labeled insulin at various concentrations of test substance and the K_d was calculated. According to this method, human insulin receptor (HIR) or human IGF-1 receptor (HIGF-1R) was purified from transfected cells after solubilization with Triton X-100. The assay buffer contained 100 mM HEPES (pH 7.8), 100 mM NaCl, 10 mM MgCl_2 , 0.5% human serum albumin (HSA), 0.2% gammaglobulin and 0.025% Triton X-100. The receptor concentration was chosen to give 30-60% binding of 2000 cpm (3 pM) of its ^{125}I -labeled ligand (TyrA14- ^{125}I -HI or Tyr31- ^{125}I -IGF1) and a dilution series of the substance to be tested was added. After equilibration for 2 days at 4°C, each sample (200 μl) was precipitated by addition of 400 μl 25% PEG 6000, centrifuged, washed with 1 ml 15% PEG 6000, and counted in a gamma-counter.

The insulin/IGF-1 competition curve was fitted to a one-site binding model and the calculated parameters for receptor concentration, insulin affinity, and non-specific binding were used in calculating the binding constants of the test substances. Representative curves for insulin competition are shown in Figures 10A-10C; 11A-11D. Qualitative data are provided in Table 4, below.

Table 4 illustrates IR affinities for the RP9 monomer peptide and various RP9 monomer truncations. The results demonstrate that RP9 N-terminal sequence (GSLD; SEQ ID NO:1785) and C-terminal sequence (LGKK; SEQ ID NO:1786) can be deleted without substantially affecting HIR binding affinity (Table 4).

TABLE 4

Peptide	SEQ ID NO:	Formula	Site IR	Sequence	HIR K_d (mol/l)
S386	1559	1	1	GSLDESFYDWFERQLG	$3.2 \cdot 10^{-7}$
S395	1787	1	1	GSLDESFYDWFERQL	$9.1 \cdot 10^{-8}$
S394	1788	1	1	GSLDESFYDWFERQ	$8.1 \cdot 10^{-8}$
S396	1789	1	1	GSLDESFYDWFER	$>2 \cdot 10^{-5}$
S399	1790	1	1	ESFYDWFERQL	$9.1 \cdot 10^{-8}$
S400	1791	1	1	ESFYDWFERQ	$6.3 \cdot 10^{-7}$

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Figures 10A-10C demonstrate that Site 1-Site 2 heterodimer peptides 537, 538, and 539 bound to IR with substantially higher (several orders of magnitude) affinity than corresponding monomer (D117 and 540) and homodimer (521 and 535) peptides. Figures 11A-11D demonstrate that Site 1-Site 2 heterodimer peptides, 537 and 538, bound to IR with markedly higher affinity than the monomer peptide D117.

Example 4: Adipocyte Assay for Determination of Insulin Agonist Activity

Insulin increases uptake of ^3H glucose into adipocytes and its conversion into lipid. Incorporation of ^3H into the lipid phase was determined by partitioning of lipid phase into a scintillant mixture, which excludes water-soluble ^3H products. The effect of compounds on the incorporation of ^3H glucose at a sub-maximal insulin dose was determined, and the results expressed as increase relative to full insulin response. The method was adapted from Moody *et al.*, 1974, *Horm Metab Res.* 6(1):12-6.

Mouse epididymal fat pads were dissected out, minced into digestion buffer (Krebs-Ringer 25 mM HEPES, 4% HSA, 1.1 mM glucose, 0.4 mg/ml Collagenase Type 1, pH 7.4), and digested for up to 1.5 h at 36.5°C. After filtration, washing (Krebs-Ringer HEPES, 1% HSA), and resuspension in assay buffer (Krebs-Ringer HEPES, 1% HSA), free fat cells were pipetted into 96-well Picoplates (Packard), containing test solution and approximately an ED_{20} insulin.

The assay was started by addition of ^3H glucose (Amersham TRK 239), in a final concentration of 0.45 mM glucose. The assay was incubated for 2 h, 36.5°C, in a Labshaker incubation tower, 400 rpm, then terminated by the addition of Permablend/Toluene scintillant (or equivalent), and the plates sealed, before standing for at least 1 h and detection in a Packard Top Counter or equivalent. A full insulin standard curve (8 dose) was run as control on each plate.

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Data are presented graphically, as effect of compound on an (approximate) ED₂₀ insulin response, with data normalized to a full insulin response. The assay can also be run at basal or maximal insulin concentration. Representative dose-response curves for insulin and IGF-1 are shown in Figures 12-18. Qualitative data are shown in Tables 5-7.

In free fat cell (FFC) assays, truncated synthetic RP9 monomer peptides S390 and S394 showed potency similar to full-length RP9 monomer peptides (Figures 12A-12D). Truncated synthetic RP9 homodimer peptides S415 and S417 were highly potent in FFC assays, but less potent than full-length RP9 homodimer peptides (Figures 13A-13C; compare to peptides 521 and 535, described below). The potency of recombinant RP9 homodimer peptides 521 and 535 in FFC assays is shown in Figures 14A-14C. The curves are flattened, suggesting that the binding mechanism may not be mediated by simple intramolecular binding (Figures 14A-14C).

Results further indicated that synthetic RP9 homodimer peptides S337 and S374 showed increased HIR binding affinity and increased potency in FFC assays compared to synthetic RP9 monomer, S371 (Table 5). Similarly, synthetic RP9 homodimer peptides S314 and S317 showed increased HIR binding affinity and increased potency in FFC assays compared to synthetic RP9 monomer, S371, and various RP9 truncations (Table 6).

TABLE 5

Pep.	SEQ ID NO:	Formula	Site IR	Monomer or Dimer	Sequence	HIR K _d (mol/l)	FFC
S371	1558	1	1	M (RP9)	GSLDESFYDWFERQLGKK	6.3*10 ⁻⁷	+
S337	1792	1-1	1-1	D, C-Term 23	(GSLDESFYDWFERQLGKK-Lig) ₂₋₂₃	1.1*10 ⁻⁸	+++++
S374	1793	1-1	1-1	D, N-Term 17	17-(GSLDESFYDWFERQLGKK) ₂	1.8*10 ⁻⁷	++++

M = monomer; D = dimer; C-Term = C-terminal linker (C-C); N-Term = N-terminal linker (N-N); 23 and 17 represent specific chemical linkers (see Table 3); For FFC: 0 is no effect, + is agonist, - is antagonist.

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TABLE 6

Peptide	SEQ ID NO:	Form.	Site IR	Mon. or Dimer	Sequence	HIR K _d (mol/l)	FFC
S371 (RP9)	1558	1	1	M	GSLDESFYDWFERQLGKK	6.3*10 ⁻⁷	+
S395	1787	1	1	M	GSLDESFYDWFERQL	9.1*10 ⁻⁸	+
S394	1788	1	1	M	GSLDESFYDWFERQ	8.1*10 ⁻⁸	++
S396	1789	1	1	M	GSLDESFYDWFER	>2*10 ⁻⁵	0
S390	1794	1	1	M	ESFYDWFERQLG	6.2*10 ⁻⁷	+
S399	1790	1	1	M	ESFYDWFERQL	9.1*10 ⁻⁸	++
S400	1791	1	1	M	ESFYDWFERQ	6.3*10 ⁻⁷	0
S415	1795	1-1	1-1	D; C-Term	(ESFYDWFERQLGK) ₂ -23	1.0*10 ⁻⁷	++++
S417	1796	1-1	1-1	D; N-Term	23-(ESFYDWFERQLG) ₂	9.2*10 ⁻⁷	+++

5 M = monomer; D = dimer; C-Term = C-terminal linker (C-C); N-Term = N-terminal linker (N-N); 23 represents a specific chemical linker (see Table 3); For FFC: 0 is no effect, + is agonist, - is antagonist; Form. = formula; Mon. = monomer;

Site 1-Site 2 dimer peptides 537 and 538 were inactive in the FFC assays using the standard concentration of insulin (Figures 15A-15C). However, Site 1-Site 2 dimer peptides 537 and 538 were antagonists in the FFC assay in the presence of a stimulating concentration of insulin (Figures 16A-16C). In contrast, Site 2-Site 1 dimer peptide 539 was a full agonist in the FFC assay, with a slope similar to that of insulin (Figures 17A-17B).

Additional experiments confirmed that FFC assay activity of Site 1-Site 2 dimer peptides was affected by the orientation of the monomer subunits (Figures 18A-18D). In particular, dimer peptides comprising Site 1 (S372 or S373) and Site 2 (S451 or S452) monomer subunits exhibited antagonist activity in the Site 1-Site 2 orientation (C-N linkage) (dimer peptide S453); moderate levels of agonist activity in the Site 1-Site 2 orientation (N-N or C-C linkage) (dimer peptides S454 and S456); and high levels of agonist activity in the Site 2-Site 1 orientation (C-N linkage) (dimer peptide S455) (Figures 18A-18D).

Table 7, below, shows the HIR binding affinity and FFC assay potency of various synthetic peptides, including Site 1-Site 1 dimer peptides S325, S329, S332; S333, S334, S335, S336, S337, S349, S350, S351,

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S352, S353, S354, S361, S362, S363, S374, S375, S376, S378, S379, S380, S381, S414, S415, S416, S417, S418, S420, and S424. These synthetic dimer peptides exhibited properties comparable to dimer peptides 521 and 535, regardless of the orientation of the monomer subunits. In particular, synthetic Site 1-Site 2 dimer peptides S425, S453, and S459 exhibited antagonist properties comparable to those of the Site 1-Site 2 dimer peptides 537 and 538. Synthetic Site 1-Site 2 dimer peptides S455, S457, and S458 exhibited agonist properties comparable to the dimer peptide 539. Synthetic Site 1-Site 2 dimer peptides S436, S437, S438, S454, S456 act as partial agonists in the FFC assay (i.e., the peptides exhibit a maximal response of less than 100% that of insulin), which is shown in the table as “++” and “+++”.

Table 7 also shows properties of truncated monomer and dimer peptides, and thereby indicates which N- or C-terminal residues can be deleted without substantial loss of HIR binding affinity (e.g., see synthetic peptides S386 through S392, S394 through S403, and S436 through S445). Notably, certain Site 2-Site 1 dimers show IR affinities of 2×10^{-11} (see, e.g., S519 and S520). These peptides are also very potent in the fat cell assay (Figures 31A-31B) and even more potent in the HIR kinase assay (Figures 32A-32B) (kinase assay described below).

TABLE 7

Peptide	SEQ ID NO:	Formula	Linkage	Site IR	Sequence	HIR Kd (mol/l)	FFC
S105	1797	F1	-	1	FHENFYDWFVRQVAKK	3.1*10 ⁻⁷	++
S106	1798	F1	-	1	FHENFYDWFVRQASKK	4.2*10 ⁻⁷	++
S107	1799	F1	-	1	FHENFYDWFVRVASKK	10.0*10 ⁻⁷	+
S108	1800	F1	-	1	FHENFYDWFVAQVSKK	7.5*10 ⁻⁷	+
S109	1801	F1	-	1	FHENFYDWFARQVSKK	2.3*10 ⁻⁷	++
S110	1802	F1	-	1	FHEAFYDWFVRQVSKK	2.2*10 ⁻⁷	++
S111	1803	F1	-	1	FHANFYDWFVRQVSKK	3.3*10 ⁻⁷	0
S112	1804	F1	-	1	FAENFYDWFVRQVSKK	6.1*10 ⁻⁷	+
S113	1805	F1	-	1	AHENFYDWFVRQVSKK	5.9*10 ⁻⁷	+
S114	1556	F1	-		fhenfydwfvrqvsck	8.3*10 ⁻⁶	0
S115	1806	F1	-	1	EFHENFYDWFVRQVSEE	6.5*10 ⁻⁷	+
S116	1807	F1	-	1	FHENFYGWFRQVSKK	1.4*10 ⁻⁶	++
S117	1808	F2	-	1	HETFYSMIRSLAK	2.7*10 ⁻⁶	0
S118	1809	F2	-	1	SDGFYNAILLS	2.4*10 ⁻⁶	+
S119	1810	F2	-	1	SLNFYDALQLLAKK	1.8*10 ⁻⁶	0
S120	1811	F2	-	1	HDPFYMMKSLK	2.0*10 ⁻⁶	0
S121	1812	F2	-	1	NSFYEARMLSSK	3.1*10 ⁻⁶	0
S122	1813	F7	-		HPTSKEIYAKLLK	9.3*10 ⁻⁶	0
S123	1814	F7	-		HPSTNQMLMKLFK	1.6*10 ⁻⁵	0
S124	1815	F7	-		HPPLSELKFLIKK	2.3*10 ⁻⁵	0
S127	1816	F2	-	1	WSDFSYFQGLD	1.2*10 ⁻⁶	0
S128	1817 and 1818	F1-F1	C-C	1-1	(FHENFYDWFVRQVSKK) ₂ -Dap	1.1*10 ⁻⁶	++
S129	1819	F2	-	1	SSNFYQALMLLS	2.9*10 ⁻⁶	0
S131	1820	F1	-	1	FHENFYDWFVRQVSKK-Lig	1.2*10 ⁻⁶	+

S137	1821	F1	-	1	HENFYGWFVRQVSKK	7.7*10 ⁻⁷	0
S145	1822 and 1823	F1-F1	C-C	1-1	(FHENFYDWFVRQVSKK) ₂ -Lys	1.5*10 ⁻⁶	++
S158	1780	F1	-	1	FHENFYDWFVRQVSK	8.1*10 ⁻⁷	+
S165	1554	F1	-	1	FYDWF	>2*10 ⁻⁵	0
S166	1824	F1	-	1	FYDWFKK	>2*10 ⁻⁵	0
S167	1825	F1	-	1	AFYDWFACK	>2*10 ⁻⁵	-
S168	1826	F1	-	1	AAAFYDWFAAAAKK	3.8*10 ⁻⁶	0
S169	1827 and 1828	F1-F1	N-N	1-1	12-(Lig-FHENFYDWFVRQVSKK) ₂	5.8*10 ⁻⁷	++
S170	1829 and 1830	F1-F1	N-N	1-1	(CGFHENFYDWFVRQVSKK) ₂ (linked at cysteines)	7.0*10 ⁻⁷	+++
S171	1831	F1	-	1	CGFHENFYDWFVRQVSKK	2.9*10 ⁻⁶	+++
S172	1832 and 1833	F1-F1	N-N	1-1	14-(Lig-FHENFYDWFVRQVSKK) ₂	4.8*10 ⁻⁶	+++
S173	1834	F3	-	1	LDALDRLMRYFEERPSL	1.2*10 ⁻⁶	0
S174	1835	F3	-	1	PLAELWAYFEHSEQRSSAH	1.6*10 ⁻⁵	0
S175	1560	F1	-	1	GRVDWLQRNANFYDWFVAELG	2.3*10 ⁻⁷	+++
S176	1836	F1	-	1	NGVERAGTGDNFYDWFVAQLH	4.7*10 ⁻⁷	+
S177	1837	F2	-	1	EHWNTVDPFYFTLFEWLRESG	2.7*10 ⁻⁶	0
S178	1838	F2	-	1	EHWNTVDPFYQYFSELLRESG	1.3*10 ⁻⁷	++
S179	1839	F1	-	1	QSDSGTVHDFRYGWFRTWAS	5.4*10 ⁻⁷	+
S180	1840	F1	-	1	AFYDWFACK	>2*10 ⁻⁵	0
S181	1841	F1	-	1	AFYDWF	>2*10 ⁻⁵	0
S182	1842	F1	-	1	AFYDWF	>2*10 ⁻⁵	0
S183	1843	F1	-	1	FYDWF	>2*10 ⁻⁵	0
S184	1844	F1	-	1	Ac-FYDWF	>2*10 ⁻⁵	0
S214	1845	F1	-	1	AFYDWFACK	>2*10 ⁻⁵	0
S215	1846	F1	-	1	AFYDWFACK	>2*10 ⁻⁵	0
S216	1847	F1	-	1	AFYDWFACK	>2*10 ⁻⁵	0
S217	1848 and 1849	F2-F2	C-C	1-1	(SDGFYNAIELLS-Lig) ₂ -14	3.9*10 ⁻⁸	++
S218	1850 and 1851	F1-F1	C-C	1-1	(AFYDWFACK-Lig) ₂ -14	1.1*10 ⁻⁵	0

S219	1852	F1	-	1	FHENAYDWFVRQVSKK	>2*10 ⁻⁵	0
S220	1853	F1	-	1	FHENFADWFVRQVSKK	>2*10 ⁻⁵	0
S221	1854	F1	-	1	FHENFYAWFVRQVSKK	1.1*10 ⁻⁶	+
S222	1855	F1	-	1	FHENFYDAFVRQVSKK	>2*10 ⁻⁵	0
S223	1856	F1	-	1	FHENFYDWA VRQVSKK	>2*10 ⁻⁵	0
S226	1857	F6	-	2	QLEEWAGVQCEVYGRECPs	1.6*10 ⁻⁶	
S227	1858	F1	-	1	CGGFHENFYDWFVRQVSKK	5.1*10 ⁻⁷	++
S228	1859 and 1860	F1-F1	N-N	1-1	(CGGFHENFYDWFVRQVSKK) ₂ (linked at cysteines)	3.6*10 ⁻⁷	++
S229	1861 and 1862	F2-F4	C-C	1-2	SDGFYNAIELLS-Lig 12	4.4*10 ⁻⁹	0
					KHLCVLEELFWGASLFGYCSGKK-Lig		
S231	1863 and 1864	F1-F1	C-C	1-1	(FHENFYDWFVRQVSKKGGG-Lig) ₂ -14	2.7*10 ⁻⁷	+
S232	1865 and 1866	F1-F1	N-N	1-1	14-(Lig-GGGFHENFYDWFVRQVSKK) ₂	3.8*10 ⁻⁷	+++
S233	1867 and 1868	F1-F2	C-C	1-1	FHENFYDWFVRQVSKK-Lig 14	2.6*10 ⁻⁷	+
					SDGFYNAIELLS-Lig		
S234	1869	F1	-	1	RVDWLQRNANFYDWFVAELG	1.3*10 ⁻⁷	++
S235	1870	F1	-	1	VDWLQRNANFYDWFVAELG	5.3*10 ⁻⁸	++
S236	1871	F1	-	1	DWLQRNANFYDWFVAELG	1.0*10 ⁻⁷	++
S237	1872	F1	-	1	WLQRNANFYDWFVAELG	8.5*10 ⁻⁷	0
S238	1873	F1	-	1	LQRNANFYDWFVAELG	8.5*10 ⁻⁷	0
S239	1874	F1	-	1	QRNANFYDWFVAELG	1.3*10 ⁻⁶	0
S240	1875	F1	-	1	RNANFYDWFVAELG	1.4*10 ⁻⁶	
S241	1876	F1	-	1	NANFYDWFVAELG	1.6*10 ⁻⁶	
S242	1877	F1	-	1	ANFYDWFVAELG	2.0*10 ⁻⁶	
S243	1878	F1	-	1	NFYDWFVAELG	2.0*10 ⁻⁶	
S244	1879	F1	-	1	GRVDWLQRNANFYDWFVAELG-Lig	2.2*10 ⁻⁷	++
S245	1880	F1	-	1	Lig-GRVDWLQRNANFYDWFVAELG	2.2*10 ⁻⁷	+

S246	1881 and 1882	F8-F1	C-C	3-1	ACAWPTYWNCGGGG-Lig 14 FHENFYDWFVRQVSKK-Lig	5.0*10 ⁻⁶	
S248	1883	F1	-	1	GRVDWLQRNANFYDWFVAEL	6.3*10 ⁻⁸	++
S249	1884	F1	-	1	GRVDWLQRNANFYDWFVAE	7.4*10 ⁻⁷	0
S250	1885	F1	-	1	GRVDWLQRNANFYDWFVA	8.9*10 ⁻⁶	0
S251	1886	F1	-	1	GRVDWLQRNANFYDWFV	5.6*10 ⁻⁶	
S252	1887 and 1888	F2-F2	C-C	1-1	(SDGFYNAIELLS-Lig) ₂ -14	4.4*10 ⁻⁷	0
S253	1889 and 1890	F1-F1	C-C	1-1	(GRVDWLQRNANFYDWFVAELG-Lig) ₂ -14	2.2*10 ⁻⁸	++
S255	1891 and 1892	F2-F2	C-C	1-1	(SDGFYNAIELLSGGG-Lig) ₂ -14	1.6*10 ⁻⁶	0
S256	1893	F6	-	2	Acy-CLEEWGASL-Tic-QCSG	9.0*10 ⁻⁶	-
S257	1894	F2	-	1	RWPNFYGYFESLLTHFS	1.4*10 ⁻⁵	0
S259	1895	F2	-	1	EGWDFYSYFSGLLASVT	7.7*10 ⁻⁶	0
S260	1896	F2	-	1	LDRQFYRYFQDLLVGFM	2.3*10 ⁻⁶	0
S261	1897	F2	-	1	WGRSFYRYFETLLAQGI	>2*10 ⁻⁵	0
S262	1898	F4	-	1	PLCFLQELFGGASLGGYCSG	1.9*10 ⁻⁵	0
S263	1899	F6	-	2	WLEQERAWIWCEIQSGCRA	>2*10 ⁻⁵	0
S264	1900	F1	-	1	IQGWEPFYGWFDVVAQMFE	1.9*10 ⁻⁷	0
S265	1901	F1	-	1	TGHRGLDEQFYWWFRDALSG	1.1*10 ⁻⁷	0
S266	1902	F6	-	2	Abu-CLEEWGASL-Tic-QCSG	>2*10 ⁻⁵	0
S268	1903	F1	-	1	RD-Hyp-FYDWFDDI	4.5*10 ⁻⁷	0
S273	1904	F1-F2	C-N	1-1	FHENFYDWFVRQVSKK-Lig-14-Lig-SDGFYNAIELLS	1.5*10 ⁻⁶	+
S278	1905	F1-derived	-	1	GFREGQRWYWFVAQVT	>2*10 ⁻⁵	0
S281	1906	F5	-		DLRVLCELFGGAYVLGYCSE	1.1*10 ⁻⁵	0
S282	1907	F4-derived	-		HLVSGEELSWWVALLGQWAR	>2*10 ⁻⁵	0
S283	1908	F4-derived	-		APVSTEELRWGALLFGQWAG	>2*10 ⁻⁵	0
S284	1909	F6-derived	-		ALEEWAWVQVRSIRSLPL	>2*10 ⁻⁵	0
S285	1910	F6-derived	-		WLEHEWAQIQCELYGRGCTY	8.3*10 ⁻⁷	

S287	1911	F1	-	1	QAPSNFYDWFVREWDEE	5.9*10 ⁻⁶	0
S288	1912	F2	-	1	QSFYDIEELLGGEWKK	4.3*10 ⁻⁶	0
S289	1913	F2	-	1	DPFYQGLWEWLRESGEE	>2*10 ⁻⁵	0
S290	1914 and 1915	F1-F1	N-N	1-1	7-(Lig-GGGFHENFYDWFVRQVSKK) ₂	9.0*10 ⁻⁷	++
S291	1916 and 1917	F1-F1	N-N	1-1	9-(Lig-GGGFHENFYDWFVRQVSKK) ₂	1.2*10 ⁻⁶	++++
S292	1918 and 1919	F1-F1	N-N	1-1	12-(Lig-GGGFHENFYDWFVRQVSKK) ₂	7.5*10 ⁻⁷	++
S293	1920 and 1921	F1-F1	N-N	1-1	13-(Lig-GGGFHENFYDWFVRQVSKK) ₂	1.2*10 ⁻⁷	++
S294	1922	F1	-	1	DWLQRNANFYDWFVAEL-Lig	1.3*10 ⁻⁷	++
S295	1923	F1	-	1	Lig-DWLQRNANFYDWFVAEL	4.8*10 ⁻⁷	+
S300	1924 and 1925	F1-F1	C-C	1-1	(DWLQRNANFYDWFVAEL-Lig) ₂ -14	5.0*10 ⁻⁸	+++
S301	1926 and 1927	F1-F1	N-N	1-1	14-(Lig-DWLQRNANFYDWFVAEL) ₂	6.4*10 ⁻⁷	+
S302	1928	F2	-	1	SDGFYNA-Acy-ELLSG	8.6*10 ⁻⁷	0
S303	1929	F2	-	1	SGPFYEE-Acy-ELLW-Alb-G	5.7*10 ⁻⁶	0
S304	1930	F2	-	1	GGSFYDD-Acy-E-Alb-LW-Alb-G	2.1*10 ⁻⁵	0
S305	1931	F2	-	1	N-Alb-PFYDE-Acy-DE-Cha-W-Alb-G	8.4*10 ⁻⁷	0
S306	1932	F1	-	1	GRVDWLQRNANFYDWFVAE-Acy-G	2.2*10 ⁻⁶	+++
S312	1933 and 1934	F1-F1	N-N	1-1	23-(Lig ² -GGGFHENFYDWFVRQVSKK) ₂	2.9*10 ⁻⁶	++
S313	1935 and 1936	F2-F2	C-C	1-1	(SDGFYNAIELLS-Lig) ₂ -23	2.4*10 ⁻⁷	
S315	1937	F1	-	1	WFYDWFWE	6.8*10 ⁻⁶	0
S316	1938	F10	-	1	WQGYAWLS	7.0*10 ⁻⁶	0
S317	1939	F10	-	1	WPGYAWLS	>2*10 ⁻⁵	0
S319	1940	F1	-	1	D-Alc-D-Alb-EFYDWFDEIPq	8.7*10 ⁻⁷	0
S320	1941	F1	-	1	KNNKEFYEWFEIGq	2.8*10 ⁻⁶	0
S321	1942	F1	-	1	YeRD-Hyp-FYDWFDEIGq	1.4*10 ⁻⁶	0
S322	1943	F1	-	1	EWDR-Hyp-FYDWFDEI-Hyp-e	7.2*10 ⁻⁷	0
S325	1944 and 1945	F1-F1	N-N	1-1	9-(Lig ² -GSLDESFYDWFERQLGKK) ₂	4.6*10 ⁻⁸	++++
S326	1600	F1	-	1	GIISQSPESFYDWFAGQVSDPWWCW	5.9*10 ⁻⁷	-
S327	1946	F2	-	1	TFYSCASLLTGTPQPNRGPWERCCK	2.1*10 ⁻⁶	-
S329	1947 and 1948	F1-F1	N-N	1-1	17-(Lig ² -FHENFYDWFVRQVSKK) ₂	2.7*10 ⁻⁶	++
S331	1949	F4	-	2	KHLCVLEELFWGASLFGYCSGKK	1.6*10 ⁻⁶	0
S332	1950 and 1951	F1-F1	C-C	1-1	(GSLDESFYDWFERQLGKK-Lig) ₂ -9	2.1*10 ⁻⁸	++++

S333	1952 and 1953	F1-F1	N-N	1-1	22-(Lig'-GSLDESFDWFERQLGKK) ₂	1.4*10 ⁻⁷	++++
S334	1954 and 1955	F1-F1	N-N	1-1	22-(Lig'-GGGFHENFYDFWFRQVSKK) ₂	1.6*10 ⁻⁶	+++
S335	1956 and 1957	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Lig') ₂ -22	9.8*10 ⁻⁸	++++
S336	1958 and 1959	F1-F1	N-N	1-1	23-(Lig'-GSLDESFDWFERQLGKK) ₂	1.5*10 ⁻⁸	+++
S337	1960 and 1961	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Lig') ₂ -23	1.1*10 ⁻⁸	+++++
S342	1962	F1	-	1	DLWFAKEDMNFYDFWFWQLR	1.8*10 ⁻⁶	0
S344	1963	F2	-	1	EHWNTVDPFYHWISELLRESGA	2.0*10 ⁻⁷	0
S345	1964	F2	-	1	EHWNTVDPFYQYFAELLRESGA	2.9*10 ⁻⁶	0
S349	1965 and 1966	F1-F1	N-N	1-1	23-(Lig'-GGGFHENFYDFWFRQVSKK) ₂	1.3*10 ⁻⁷	++++
S350	1967 and 1968	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Lig') ₂ -21	4.7*10 ⁻⁷	++++
S351	1969 and 1970	F1-F1	N-N	1-1	21-(Lig'-GSLDESFDWFERQLGKK) ₂	1.4*10 ⁻⁶	+++
S352	1971 and 1972	F1-F1	N-N	1-1	21-(Lig'-GGGFHENFYDFWFRQVSKK) ₂	6.6*10 ⁻⁷	+++
S353	1973 and 1974	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Lig') ₂ -14	1.1*10 ⁻⁸	+++++
S354	1975 and 1976	F1-F1	N-N	1-1	14-(Lig'-GSLDESFDWFERQLGKK) ₂	3.9*10 ⁻⁸	++++
S359	1977 and 1978	F1-F1	N-N	1-1	9-(Lig'-DWLQRNANFYDFWFAEL) ₂	7.0*10 ⁻⁷	+
S360	1979 and 1980	F1-F1	N-N	1-1	23-(Lig'-DWLQRNANFYDFWFAEL) ₂	9.9*10 ⁻⁷	
S361	1981 and 1982	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Lig') ₂ -24	2.2*10 ⁻⁶	+++
S362	1983 and 1984	F1-F1	N-N	1-1	24-(Lig'-GSLDESFDWFERQLGKK) ₂	1.1*10 ⁻⁷	++++
S363	1985 and 1986	F1-F1	N-N	1-1	24-(Lig'-GGGFHENFYDFWFRQVSKK) ₂	2.2*10 ⁻⁷	+++
S365	1987	F1	-	1	RMYSFGAPQNFYDFWFWQEW	1.0*10 ⁻⁵	0
S366	1988	F1	-	1	PLRESNFYDFWFWQLE	3.7*10 ⁻⁷	0
S368	1989	F2	-	1	RGTRSDPFYHKLSELLQGH	>2*10 ⁻⁵	0
S371	1958	F1	-	1	GSLDESFDWFERQLGKK	6.3*10 ⁻⁷	+
S372	1990	F1	-	1	SGSLDESFDWFERQLGKK	2.0*10 ⁻⁷	++
S373	1991	F1	-	1	GSLDESFDWFERQLGKK(S)	1.2*10 ⁻⁷	+++
S374	1992 and 1993	F1-F1	N-N	1-1	17-(Aid-GSLDESFDWFERQLGKK) ₂	1.8*10 ⁻⁷	++++
S375	1994	F1-F1	C-N	1-1	(GSLDESFDWFERQLGKK-Aid)-14-(Aid-GSLDESFDWFERQLGKK)	2.0*10 ⁻⁷	++++
S376	1995 and 1996	F1-F1	N-N	1-1	19-(Aid-GSLDESFDWFERQLGKK) ₂	1.6*10 ⁻⁷	++++
S378	1997 and 1998	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Aid) ₂ -17	6.5*10 ⁻⁸	+++++
S379	1999 and 2000	F1-F1	C-C	1-1	(GSLDESFDWFERQLGKK-Aid) ₂ -19	5.6*10 ⁻⁸	+++++
S380	2001 and 2002	F1-F1	C-C	1-1	(EEDWLQRNANFYDFWFAEL-Lig') ₂ -9	5.1*10 ⁻⁷	++
S381	2003 and 2004	F1-F1	C-C	1-1	(EEDWLQRNANFYDFWFAEL-Lig') ₂ -23	1.2*10 ⁻⁷	++++

S386	1559	F1	-	1	GSLDESFDWFERQLG	3.2*10 ⁻⁷	+
S387	2005	F1	-	1	SLDESFDWFERQLG	6.3*10 ⁻⁷	+
S388	2006	F1	-	1	LDESFDWFERQLG	3.4*10 ⁻⁷	+
S389	2007	F1	-	1	DESFDWFERQLG	1.1*10 ⁻⁶	+
S390	1794	F1	-	1	ESFDWFERQLG	6.2*10 ⁻⁷	+
S391	2008	F1	-	1	SFDWFERQLG	1.5*10 ⁻⁶	+
S392	2009	F1	-	1	FYDWERQLG	3.8*10 ⁻⁶	0
S394	1788	F1	-	1	GSLDESFDWFERQ	9.1*10 ⁻⁸	+
S395	1787	F1	-	1	GSLDESFDWFERQL	8.1*10 ⁻⁸	++
S396	1789	F1	-	1	GSLDESFDWFER	>2*10 ⁻⁵	0
S397	2010	F1	-	1	GSLDESFDWFE	>2*10 ⁻⁵	0
S398	2011	F1	-	1	GSLDESFDWF	>2*10 ⁻⁵	0
S399	1790	F1	-	1	ESFDWFERQL	9.5*10 ⁻⁸	++
S400	1791	F1	-	1	ESFDWFERQ	6.3*10 ⁻⁷	0
S401	2012	F1	-	1	ESFDWFER	>2*10 ⁻⁵	0
S402	2013	F1	-	1	ESFDWFE	>2*10 ⁻⁵	0
S403	2014	F1	-	1	ESFDWF	>2*10 ⁻⁵	0
S414	2015 and 2016	F1-F1	C-C	1-1	(ESFDWFERQLGK-Lig') ₂ -14	3.8*10 ⁻⁷	+++
S415	2017 and 2018	F1-F1	C-C	1-1	(ESFDWFERQLGK-Lig') ₂ -23	1.0*10 ⁻⁷	+++
S416	2019 and 2020	F1-F1	N-N	1-1	14-(Lig'-ESFDWFERQLG) ₂	9.3*10 ⁻⁷	+++
S417	2021 and 2022	F1-F1	N-N	1-1	23-(Lig'-ESFDWFERQLG) ₂	9.2*10 ⁻⁷	+++
S418	2023 and 2024	F1-F1	C-C	1-1	(ESFDWFERQLGK-Ad) ₂ -17	1.2*10 ⁻⁷	+++
S419	2025 and 2026	F6-F6	N-N	2-2	14-(Lig'-EWLDQEWAWVQCEVYGRGCPSEE) ₂		0
S420	2027 and 2028	F1-F1	N-N	1-1	17-(Ad-ESFDWFERQLG) ₂		++
S423	2029 and 2030	F1-F8	C-C	1-3	ESFDWFERQLG K ACAWPTYWNCG	6.2*10 ⁻⁸	0
S425	2031	F1-F6	C-N	1-2	GSLDESFDWFERQLGKK-Lig'-14-Lig'-EWLDQEWAWVQCEVYGRGCPSEE	2.4*10 ⁻⁹	-
S429	2032	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSEE-Lig'-14-Lig'-GSLDESFDWFERQLGKK	6.0*10 ⁻¹⁰	
S432	2033 and 2034	F1-F6	C-C	1-2	ESFDWFERQLGGGG K CEVYGRGCP	1.8*10 ⁻⁷	+
S433	2035 and 2036	F1-F6	C-C	1-2	ESFDWFERQLGGGG	1.1*10 ⁻⁷	+

S436	2037 and 2038	F1-F6	C-C	1-2	WLDQEWAWVQ K ESFYDWFERQLGGG	5.2*10 ⁻¹⁰	+++
S437	2039 and 2040	F1-F6	C-C	1-2	WLDQEWAWVQCEVYGRGCP K ESFYDWFERQLGGG	6.9*10 ⁻¹⁰	+++
S438	2041 and 2042	F1-F6	C-C	1-2	LDQEWAWVQCEVYGRGCP K ESFYDWFERQLGGG	3.0*10 ⁻⁸	++
S439	2043 and 2044	F1-F6	C-C	1-2	DQEWAWVQCEVYGRGCP K ESFYDWFERQLGGG	4.6*10 ⁻⁸	
S440	2045 and 2046	F1-F6	C-C	1-2	QEWAWVQCEVYGRGCP K ESFYDWFERQLGGG	9.9*10 ⁻⁸	
S441	2047 and 2048	F1-F6	C-C	1-2	EWAWVQCEVYGRGCP K ESFYDWFERQLGGG	1.2*10 ⁻⁷	
S442	2049 and 2050	F1-F6	C-C	1-2	WAWVQCEVYGRGCP K ESFYDWFERQLGGG	1.6*10 ⁻⁷	
S443	2051 and 2052	F1-F6	C-C	1-2	AWVQCEVYGRGCP K ESFYDWFERQLGGG	1.7*10 ⁻⁷	
S444	2053 and 2054	F1-F6	C-C	1-2	WVQCEVYGRGCP K ESFYDWFERQLGGG	1.9*10 ⁻⁷	
S445	2055 and 2056	F1-F6	C-C	1-2	VQCEVYGRGCP K ESFYDWFERQLGGG	2.3*10 ⁻⁷	
S453	2057	F1-F6	C-N	1-2	QCEVYGRGCP K GSLDESFYDWFERQLGKKK-Ald-17-Ald-KEWLDOEWAWVQCEVYGRGCPSEE	5.7*10 ⁻¹⁰	-

S454	2058 and 2059	F1-F6	C-C	1-2	GSLDESFDWFERQLGKK-Aid-17 EWLDQEWAWVQCEVYGRGCPSEEK-Aid-17	3.8*10 ⁻¹⁰	+++
S455	2060	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSEEK-Aid-18-Aid-GSLDESFDWFERQLGKK	1.1*10 ⁻⁹	++++
S456	2061 and 2062	F1-F6	N-N	1-2	Aid-GSLDESFDWFERQLGKK 17 Aid-KEWLDQEWAWVQCEVYGRGCPSEE	2.4*10 ⁻⁹	+++
S457	2063	F6-F1	C-N	2-1	WLDQEWAWVQCEVYGRGCPSSGGSGSLDESFDWFERQLG	1.6*10 ⁻⁹	++++
S458	2064	F6-F1	C-N	2-1	WLDQEWAWVQCEVYGRGCPSSGGSGSLDESFDWFERQLG	3.2*10 ⁻⁹	++++
S459	2065	F1-F6	C-N	1-2	GSLDESFDWFERQLGSGSGSWLDQEWAWVQCEVYGRGCPSS	7.6*10 ⁻¹¹	-
S467	2066	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSEEK-Aid-16-Aid-GSLDESFDWFERQLGKK	6.8*10 ⁻¹⁰	++++
S468	2067	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSEEK-Aid-19-Aid-GSLDESFDWFERQLGKK	4.0*10 ⁻¹⁰	++++
S471	2068	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG	6.7*10 ⁻¹⁰	++++
S481	2069	F6-F1	C-N	2-1	HHHHHKLQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S482	2070	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S483	2071	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG	5.2*10 ⁻⁸	0
S484	2072	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG	8.7*10 ⁻⁸	0
S485	2073	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG	1.6*10 ⁻⁷	0
S486	2074	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG	5.7*10 ⁻⁸	0
S487	2075	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S488	2076	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S489	2077	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S490	2078	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S491	2079	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S492	2080	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S493	2081	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSEE-POX-Lys(biotin)		
S494	2082	F6-F1	C-N	2-1	ADQEWAWVQCEVYGRGCPSESYFDWFERQLG	1.7*10 ⁻⁸	+
S495	2083	F6-F1	C-N	2-1	LAQEWAWVQCEVYGRGCPSESYFDWFERQLG		
S496	2084	F6-F1	C-N	2-1	LDAEWAWVQCEVYGRGCPSESYFDWFERQLG		
S497	2085	F6-F1	C-N	2-1	LDQAWAWVQCEVYGRGCPSESYFDWFERQLG	2.5*10 ⁻⁹	+++
S498	2086	F6-F1	C-N	2-1	LDQEAAWVQCEVYGRGCPSESYFDWFERQLG	5.6*10 ⁻⁸	+
S499	2087	F6-F1	C-N	2-1	LDQEWAAVQCEVYGRGCPSESYFDWFERQLG	6.2*10 ⁻¹⁰	++++

S500	2088		F6-F1	C-N	2-1	LDQEWAWAQCEVYGRGCPSESYDWFERQL		
S501	2089		F6-F1	C-N	2-1	LDQEWAWACEVYGRGCPSESYDWFERQL		
S502	2090		F6-F1	C-N	2-1	LDQEWAWQCAVYGRGCPSESYDWFERQL	3.0*10 ⁻⁹	+++
S503	2091		F6-F1	C-N	2-1	LDQEWAWQCEAYGRGCPSESYDWFERQL		
S504	2092		F6-F1	C-N	2-1	LDQEWAWQCEVAGRGCPSESYDWFERQL		
S505	2093		F6-F1	C-N	2-1	LDQEWAWQCEVARGCPSESYDWFERQL		
S506	2094		F6-F1	C-N	2-1	LDQEWAWQCEVYAGCPSESYDWFERQL		
S507	2095		F6-F1	C-N	2-1	LDQEWAWQCEVYGRACPSSESYDWFERQL		
S508	2096		F6-F1	C-N	2-1	LDQEWAWQCEVYGRGCASESYDWFERQL		
S509	2097		F6-F1	C-N	2-1	LDQEWAWQCEVYGRGSPSESYDWFERQL		
S510	2098		F6-F1	C-N	2-1	SLEEWAQCEVYGRGCPGGSGGLLDESFYHWFDRQLR	6.2*10 ⁻¹¹	++++
S511	2099		F6-F1	C-N	2-1	WLDQEWAWQCEVYGRGCPGGSGGRVDWLQRNANFYDWFVAELG	3.8*10 ⁻⁹	++
S512	2100		F6-F1	C-N	2-1	WLDQEWAWQCEVYGRGCPGGSGGSAFYAWFDQVLRTV	2.8*10 ⁻⁸	++
S513	2101		F6-F1	C-N	2-1	WLDQEWAWQCEVYGRGCPGGSGGSDAFYSGLWALIGLSDG		
S515	2102		F6	.	2	LDQEWAWQCEVYGRGCPSPGX-Lys(Biotin)		
S516	2103		F4-F1	C-N	2-1	H-Acy-CLEEWGASL-Tic-QCSGSESYDWFERQL		
S517	2104		F6-F1	C-N	2-1	SIEEWAQIKDVGWGRGCPSESYDWFERQL		
S518	2105		F6-F1	C-N	2-1	RLEEWAWWQCEVYGRGCPGSLDESFDWFERQLG	1.6*10 ⁻¹⁰	++++
S519	2106		F6-F1	C-N	2-1	SLEEWAQCEVYGRGCPGSLDESFDWFERQLG	2.0*10 ⁻¹¹	++++++
S520	2107		F6-F1	C-N	2-1	SIEEWAQIKDVGWGRGCPGLLDESFYHWFDRQLR	2.0*10 ⁻¹¹	++++++
S521	2108		F4-F1	C-N	2-1	HLCVLEELFWGASLFGYCSGSLDESFDWFERQL	2.7*10 ⁻⁸	+
S522	2109		F4-F1	C-N	2-1	HLCVLEELFWGASLFGYCSGGRVDWLQRNANFYDWFVAELG		
S523	2110		F6-F10	C-N	2-1	WLDQEWAWWQCEVYGRGCPSDSDWAGYEWFEQLD	4.3*10 ⁻⁹	++
S524	2111		F6-F1	C-N	2-1	HHHHHKSLEEWAQCEVYGRGCPGSLDESFDWFERQLG		

S471	2068		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG	6.7*10 ⁻¹⁰	++++
S481	2069		F6-F1	C-N	2-1	HHHHHKLQDEWAWWQCEVYGRGCPSESYDWFERQLG	1.3 * 10 ⁻⁹	
S482	2070		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG		
S483	2071		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG	5.2*10 ⁻⁸	0
S484	2072		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG	8.7*10 ⁻⁸	0
S485	2073		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG	1.6*10 ⁻⁷	0
S486	2074		F6-F1	C-N	2-1	LDQEWAWWQCEVYGRGCPSESYDWFERQLG	5.7*10 ⁻⁸	0

S487	2075	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S488	2076	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S489	2077	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S490	2078	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S491	2079	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S492	2080	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S493	2081	F6-F1	C-N	2-1	EWLDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S494	2082	F6-F1	C-N	2-1	ADQEWAWVQCEVYGRGCPSESYDWFERQLG	1.7*10 ⁻⁹	+
S495	2083	F6-F1	C-N	2-1	LAQEWAWVQCEVYGRGCPSESYDWFERQLG	2.6*10 ⁻⁹	
S496	2084	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S497	2085	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	2.5*10 ⁻⁹	+++
S498	2086	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	5.6*10 ⁻⁹	+
S499	2087	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	6.2*10 ⁻¹⁰	++++
S500	2088	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S501	2089	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S502	2090	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	3.0*10 ⁻⁹	+++
S503	2091	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	2.1*10 ⁻⁹	
S504	2092	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	1.3*10 ⁻⁸	
S505	2093	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S506	2094	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S507	2095	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S508	2096	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S509	2097	F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQLG	5.7*10 ⁻⁹	
S510	2098	F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFERQLG	6.2*10 ⁻¹¹	+++++
S511	2099	F6-F1	C-N	2-1	WLDQEWAWVQCEVYGRGCPSESYDWFERQLG	3.8*10 ⁻⁹	++
S512	2100	F6-F1	C-N	2-1	WLDQEWAWVQCEVYGRGCPSESYDWFERQLG	2.8*10 ⁻⁹	++
S513	2101	F6-F1	C-N	2-1	WLDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S515	2102	F6	-	2	LDQEWAWVQCEVYGRGCPSESYDWFERQLG		
S516	2103	F4-F1	C-N	2-1	H-Acy-CLEEWGASL-Tic-QCSGSESYDWFERQLG		
S517	2104	F6-F1	C-N	2-1	SIEEEWAQIKCDVWGRGCPSESYDWFERQLG	6.0*10 ⁻¹²	+++++
S518	2105	F6-F1	C-N	2-1	RLEEEWAQVECEVYGRGCPSESYDWFERQLG	1.6*10 ⁻¹⁰	+++++
S519	2106	F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFERQLG	2.0*10 ⁻¹¹	+++++
S520	2107	F6-F1	C-N	2-1	SIEEEWAQIKCDVWGRGCPSESYDWFERQLG	2.0*10 ⁻¹¹	+++++
S521	2108	F4-F1	C-N	2-1	HLCVLEELFWGASLFGYCSGGSLDESFDWFERQLG	2.7*10 ⁻⁸	+
S522	2109	F4-F1	C-N	2-1	HLCVLEELFWGASLFGYCSGGSLDESFDWFERQLG		

S523	2110	F6-F10	C-N	2-1	WLDQEWAWVQCEVYGRGCPSSDWDAGYEWFEELD	4.3*10 ⁻⁹	++
S524	2111	F6-F1	C-N	2-1	HHHHHKSLEEEWAQVECEVYGRGCPSSLDSEFYDWFERQLG	1.1*10 ⁻¹¹	+++++
S527		F4-F1	C-N	2-1	H-Acy-CAQEWGSEL-Tic-QCSGSESYDWFERQL	2.4*10 ⁻⁹	
S530		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFERQL	8.0*10 ⁻¹²	+++++
S531		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSEFYDWFERQL	7.5*10 ⁻¹¹	+++
S532		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSSLDSEFYDWFERQL	3.7*10 ⁻¹¹	+++++
S533		F6-F1	C-N	2-1	LDQEWAWVQCEVYGRGCPSESYDWFERQL	6.7*10 ⁻¹¹	+++
S534		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFERQL	1.0*10 ⁻¹¹	+++++
S535		F6-F1	C-N	2-1	QLDEEWAGVQCEVYGRGCPSSLDSEFYDWFERQLG		
S536		F6-F1	C-N	2-1	LEEEWAQVECEVYGRGCPSESYDWFERQL	8.3*10 ⁻¹¹	++++
S537		F6-F1	C-N	2-1	SLEHEWAQVECEVYGRGCPSSLDSEFYDWFERQLG	4.4*10 ⁻¹¹	++++
S538		F6-F1	C-N	2-1	SLEQEWAWVQCEVYGRGCPSSLDSEFYDWFERQLG	3.8*10 ⁻¹¹	++++
S539		F6-F1	C-N	2-1	SLELEWAQVECEVYGRGCPSSLDSEFYDWFERQLG	9.8*10 ⁻¹¹	++++
S540		F6-F1	C-N	2-1	SLEEEWAQVKEVYGRGCPSSLDSEFYDWFERQLG	1.3*10 ⁻¹¹	+++++
S541		F6-F1	C-N	2-1	SLEEEWAQVECEVWGRGCPSSLDSEFYDWFERQLG	7.8*10 ⁻¹²	+++++
S542		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSSLDSEFYDWFERQLG	2.7*10 ⁻¹¹	+++++
S543		F1-F6	C-N	1-2	GSLDESYDWFERQLGGGGGSLDEEWAQVQCEVYGRGCPSS	1.9*10 ⁻¹¹	---
S544		F1-F6	C-N	1-2	ESFYDWFERQLGWLQDEWAWVQCEVYGRGCPSS		
S545		F1-F6	C-N	1-2	ESFYDWFERQLGWLDEEWAQVQCEVYGRGCPSS		
S546		F6-F1	C-N	2-1	SLEEEWAQVECEV-Bpa-GRGCPSSLDSEFYDWFERQ-Bpa-GK(Biotin)	2.6*10 ⁻⁸	
S547		F6		2	SLEEEWAQVECEVYGRGCPSS	4.9*10 ⁻⁸	-
S548		F6		2	SLEEEWAQVECEVWGRGCPSS	4.1*10 ⁻⁹	-
S549		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSSLDSEFYDWFERQLG	1.3*10 ⁻¹¹	+++++
S550		F1		1	Ac-GSLDESYDWFERQLG-POX-K	4.0*10 ⁻⁸	
S551		F6-F1	C-N	2-1	SLEEEWAQVEAEVYGRGCPSSLDSEFYDWFERQLG	7.2*10 ⁻¹¹	
S552		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSSLDSEFYDWFERQLGKHHHHH		
S553		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPPLDSEFYDWFDRQLR	7.3*10 ⁻¹²	
S554		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFERQLG	6.4*10 ⁻¹²	+++++
S555		F6-F1	C-N	2-1	SLEEEWAQVECEVYGRGCPSESYDWFVRQLG	5.7*10 ⁻¹¹	++++
S556		F6-F1	C-N	2-1	SLEEEWAQIKCDWVGRGCPSESYDWFERQL	3.2*10 ⁻¹¹	++++

S557		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	2.0*10 ⁻¹¹	+++++
S558		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.9*10 ⁻¹¹	+++++
S559		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	2.1*10 ⁻¹¹	+++++
S560		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.4*10 ⁻¹¹	+++++
S561		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.8*10 ⁻¹¹	+++++
S562		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.8*10 ⁻¹¹	++++
S563		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.4*10 ⁻¹¹	++++
S564		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.3*10 ⁻¹¹	++++
S565		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S566		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S567		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S568		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	4.3*10 ⁻¹²	+++++
S569		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.5*10 ⁻¹⁰	+++
S570		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	7.3*10 ⁻¹⁰	+++
S571		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.6*10 ⁻⁹	
S572		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	4.8*10 ⁻⁹	
S573		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	3.6*10 ⁻¹¹	+++
S574		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	9.2*10 ⁻¹²	++++
S575		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S576		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S577		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S578		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S579		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S580		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.2*10 ⁻¹¹	++++
S581		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.2*10 ⁻¹¹	+++
S582		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	2.5*10 ⁻⁹	
S583		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S584		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	9.3*10 ⁻⁹	
S585		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S586		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S587		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S588		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.8*10 ⁻¹⁰	++++
S589		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL		
S590		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	5.8*10 ⁻¹¹	++++
S591		F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.3*10 ⁻¹⁰	++++
S592		F6		2	SLEEWAQIECEVWGRGCPSESYDWFERQL	1.7*10 ⁻⁹	

S593	F6		2	SIEEWAQIKCDWGRGCPSY	2.2*10 ⁻⁹	
S594	F6-F1	C-N	2-1	SLEEWAQIECEVWGRGWHSFYDWFERQL	7.1*10 ⁻¹¹	++++
S595	F6-F1	C-N	2-1	LEEEWAQIREVWHSFASFYDWFERQL	6.2*10 ⁻¹⁰	+++
S596	F6-F1	C-N	2-1	SLEEWAQIQHLYGPAESFYDWFERQL	4.5*10 ⁻¹¹	+++
S597	F6-F1	C-N	2-1	Ac-SLEEWAQIECEVYGRGCPSEFYDWFERQL	8.5*10 ⁻¹²	++++++
S600	F6-F1	C-N	2-1	Ac-SIEEWAQIKCDWGRGSEFYDWFERQL	7.6*10 ⁻¹²	
S601	F6-F1	C-N	2-1	SLEEWAQIQEDLYGANHNEFYDWFERQL	1.8*10 ⁻¹⁰	
S602	F6-F1	C-N	2-1	SLEEWAQIOAEVYGNPSEFYDWFERQL	3.1*10 ⁻¹¹	
S603	F6-F1	C-N	2-1	Ac-SLEEWAQIQEDLYGANHNEFYDWFERQL	1.5*10 ⁻¹¹	
S604	F6-F1	C-N	2-1	SLEEWAQIQCEVWGRGCVRRHFDWFERQL		
S605	F6-F1	C-N	2-1	SLEEWAQIQHLYWVPEKSEFYDWFERQL	9.4*10 ⁻¹¹	+++
S606	F6-F1	C-N	2-1	SLEEWAQIQCEVWGRGCPSEFYDWFERQL	4.0*10 ⁻¹²	++++++
S607	F6-F1	C-N	2-1	SLEEWAQIQCKLYGRNCKSEFYDWFERQL		
S608	F6-F1	C-N	2-1	SLEEWAQIQCKWKGCKSEFYDWFERQL		
S609	F6-F1	C-N	2-1	SLEEWAQIQCKLYGRNCKSEFYDWFERQL		
S610	F6-F1	C-N	2-1	SLEEWAQIQCKLWGNCKSEFYDWFERQL		
S611	F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSEFYDWFERQLPK		
S612	F6-F1	C-N	2-1	HQLEEWQAIQCELVWGRGCPSEFYDWFERQL		
S613	F6-F1	C-N	2-1	HLEEWSEIQCELVWGRGCPSEFYDWFERQL		
S614	F6-F1	C-N	2-1	SLEEWAQIECEVYGRGCPSEFYDWFEAQLHA		
S615	F6-F1	C-N	2-1	Ac-SLEEWAQIECEVYGRGCPSEFYDWFEAQLHA		
S616	F6-F1	C-N	2-1	HQLEEWQAIQCELVWGRGCPSEFYDWFEAQLHA		
S617	F6-F1	C-N	2-1	HLEEWSEIQCELVWGRGCPSEFYDWFEAQLHA		
S618	F6-F1	C-N	2-1	HELEEWKRIECLWGRGCPSEFYDWFEAQLHA		
S619	F6-F1	C-N	2-1	Ac-HQLEEWQAIQCELVWGRGCPSEFYDWFEAQLHA		
S620	F6-F1	C-N	2-1	Ac-HLEEWSEIQCELVWGRGCPSEFYDWFEAQLHA		
S621	F6-F1	C-N	2-1	Ac-HELEEWKRIECLWGRGCPSEFYDWFEAQLHA		
S622	F6-F1	C-N	2-1	SLEEWAQIECEVWGRGCPSEFYDWFERQLG		
S623	F6-F1	C-N	2-1	Ac-SLEEWAQIECEVWGRGCPSEFYDWFERQLG		
S624	F6-F1	C-N	2-1	SLEEWAQIECEV-(3-Iodo-Tyr)-GRGCPSSLDSEFYDWFERQLG-NH2		
S625	E8		1	KVRGFGGTWPGYEWLRNAKK		
S626	F6-E8	C-N	2-1	SLEEWAQIECEVYGRGCPSVRGFGGTWPGYEWLRNA		
S627	F6-F1	C-N	2-1	Ac-SLEEWAQIQHLYWVPEKSEFYDWFERQL		
S628	F6-F1	C-N	2-1	Ac-HQLEEWQAIQHLYWVPEKSEFYDWFEAQLHA		
S629	F6-F1	C-N	2-1	HLEEWQAIQCELVWGRGCPSEFYDWFERQL		
S630	F6-F1	C-N	2-1	Ac-HLEEWQAIQCELVWGRGCPSEFYDWFEAQLHA		

S631		F6-F1	C-N	2-1	HPLLEEWSQLQCELVWGRGCPSESYDFWFERQL	
S632		F6-F1	C-N	2-1	Ac-HPLLEEWSQLQCELVWGRGCPSESYDFWFEAQLHA	
S633		F6-F1	C-N	2-1	HGLEEEWAQIQCEVWGRGCPSESYDFWFEAQLHA	
S634		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCPSESYDFWFEAQLHA	
S635		F6-F1	C-N	2-1	Ac-SLEEEWAQIECEVYGRGCPSEDFYDFWFEELHN	
S636		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCPSESYDFWFERQL	
S637		F6-F2	C-N	2-1	Ac-SLEEEWAQIECEVYGRGCPSDGFYNAILLS	
S638		F6-F1	C-N	2-1	Ac-HGLEEEWAQIQCEVWGRGCPPEPFYDFWFEAQLHA	
S639		F6-F1	C-N	2-1	Ac-HGLEEEWAQIQCEVWGRGCPSESYDFWFEAQLHA	
S640		F6		2	SLEEEWAQIQHELWPVEAGESY	
S641		F6-F1	C-N	2-1	Ac-SLEEEWAQIQAEVWGRGAPSESYDFWFEAQLHA	
S642		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCPPEPFYDFWFERQL	
S643		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCELVWGRGCPSESYDFWFERQL	
S644		F6-F1	C-N	2-1	SLEEEWAQHEEDVYHPPAESYDFWFERQL	
S645		F6-F1	C-N	2-1	Ac-HGLEEEWAQHEEDVYHPPAESYDFWFEAQLHA	
S646		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCHNHLPFYDFWFERQL	
S647		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCPSEPFYDFWFAHDNGD	
S648		F6-F1	C-N	2-1	Ac-SLEEEWAQIQCEVWGRGCPSEAFYDFWFAEQLDD	

7, 9, 12, 13, 14, 17, 19, 20, 21, 22, 23, and 24 represent specific chemical linkers (see Table 3); For FFC: 0 is no effect, + is agonist, - is antagonist. Peptides listed on 3 lines consist of two different peptides, linked N-N or C-C, either by chemical linkage or by being synthesized on the two branches of an amino acid with two amino groups such as, e.g., lysine. Acy = 1-amino-1-cyclohexanecarboxylic acid; Cha = cyclohexylalanine; Alb = 2-aminoisobutyric acid; Hyp = Hydroxyproline; Amino acids which are not capitalized are D-amino acids; Lig = Diaminopropionic acid with a 2-aminohydroxyacetyl group (CO-CH₂-O-NH₂) on the side chain amino group; Lig' = lysine with a 2-aminohydroxyacetyl group (CO-CH₂-O-NH₂) on the side chain amino group; Ald = an aldehyde group obtained by periodate oxidation of a serine, either N-terminal or attached to the side chain amino group of lysine.

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Results further indicated that S175-S175 dimer peptides (Site 1-Site 1) were less agonistic than S175 monomer peptides (++ vs. +++). S175-S175 dimer peptides having a C-N linkage were less agonistic or equally agonistic as compared to S175-S175 dimer peptides having C-C or N-N linkages. F8-F8 dimer peptides, like the parent monomer, showed no agonist activity.

Table 7 further indicates that, relative to peptide S519, a potent insulin mimetic, the alterations that are most influential in increasing receptor affinity and potency are: acetylation of the N-terminal amino group; replacing V at position 9 with I; replacing E at position 10 with Q; replacing Y at position 14 with W; and deleting the sequence GSLD at positions 21 to 24.

Example 5: Substrate Phosphorylation Assay (HIR Kinase)

WGA (wheat germ agglutinin)-purified recombinant human insulin receptor was mixed with either insulin or peptide in varying concentrations in substrate phosphorylation buffer (50 mM HEPES (pH 8.0), 3 mM MnCl_2 , 10 mM MgCl_2 , 0.05 % Triton X-100, 0.1 % BSA, 12.5 μM ATP). A synthetic biotinylated substrate peptide (Biotin-KSRGDYMTMQIG) was added to a final concentration of 2 $\mu\text{g}/\text{ml}$. Following a 1 hr incubation at RT, the reactions were stopped by the addition of 50 mM EDTA. The reactions were transferred to Streptavidin coated 96-well microtiter plates (NUNC, Cat. No. 236001) and incubated for 1 hr at RT. The plates were washed 3 times with TBS (10 mM Tris (pH 8.0), 150 mM NaCl).

Subsequently, a 2000-fold dilution of horseradish peroxidase (HRPO) conjugated phosphotyrosine antibody (Transduction Laboratories, Cat. No. E120H) in TBS was added. The plates were incubated for 30 min and washed 3 times with TBS. TMB (3,3',5,5'-tetramethylbenzidine; Kem-En-Tec, Copenhagen, Denmark) was added. One substrate from Kem-En-Tec was added. After 10-15 min, the reaction was stopped by the addition of 1% acetic acid. The absorbance, representing the extent of substrate

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phosphorylation, was measured in a spectrophotometer at a wavelength of 450 nM.

The results indicated that the potency of the Site 1-Site 2 dimer, peptide 539, was 0.1 to 1% of that of insulin in all assays tested (Table 8), and the dose-response curves (Figures 17A-17B) had a shape similar to that of insulin dose-response curves, suggesting an insulin-like action mechanism. In addition, Site 1-Site 2 dimer peptides 537 and 538 were also active as specific insulin receptor antagonists (Table 8; Figures 16A-16C). Notably, Site 2-Site 1 dimer peptide 539 was more active in the kinase assay than Site 1-Site 1 homodimer peptides 521 and 535 (Figures 19A-19B), despite lower FFC potency (Figures 14A-14C; Figures 17A-17B). Similar results are shown in Figures 20A-B and Figures 21A-B. This data suggested that homodimer and heterodimer peptides used different mechanisms of action.

15

TABLE 8

Pep.	Mon./ Link.	Sequence	SEQ ID NO:	Form	Site IR	HIR K _d (nM)	HIGF-1R K _d (nM)	FFC Pot. (nM)	Kinase Pot. (nM)
HI				na	na				
HIGF-1R				na	na				
521	RP9-6aa-RP9	MADYKDDDDKGS�DESFDWFERQLGKKGGSGGSGSLDESFDWFERQLGKKAAA(ETAG)PG	2112	1-1	1-1	25	-	A 3	1400
535	RP9-12aa-RP9	MADYKDDDDKGS�DESFDWFERQLGKKGGSGGSGGSGGSGSLDESFDWFERQLGKKAAA(ETAG)PG	2113	1-1	1-1	15	-	A 2	1000
537	RP9-6aa-D8	MADYKDDDDKGS�DESFDWFERQLGKKGGSGGSGGSGGSGSLDQEWAWVQCEVYGRGCPAAAA(ETAG)PG	2114	1-6	1-2	0.092	980	N 10	Inactive
538	RP9-12aa-D8	MADYKDDDDKGS�DESFDWFERQLGKKGGSGGSGGSGGSGSLDQEWAWVQCEVYGRGCPAAAA(ETAG)PG	2115	1-6	1-2	0.080	710	N 10	Inactive
539	D8-6aa-RP9	MADYKDDDDKWLQEWAWVQCEVYGRGCPGGSGGSGSLDESFDWFERQLGKKAAA(ETAG)PG	2116	6-1	2-1	0.530	1500	A 10	110

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A = agonist; N = antagonist; na = not applicable; Form. = formula; Mon. = constituent monomers; Link. = linker; Pot. = potency; HI and HIGF-1R are controls; All with tags at both ends; All dimers are linked C-N; Linker sequences are underlined.

Example 6: IR Autophosphorylation Assays

5 IR activation was assayed by detecting autophosphorylation of an insulin receptor construct transfected into 32D cells (Wang *et al.*, 1993, *Science* **261**:1591-1594; clone 969). The IR transfected 32D cells were seeded at 5×10^6 cells/well in 96-well tissue culture plates and incubated overnight at 37°C. Samples were diluted 1:10 in the stimulation medium
10 (PRIM1640 with 25 nM HEPES pH 7.2) plus or minus insulin. The culture media was decanted from the cell culture plates, and the diluted samples were added to the cells. The plates were incubated at 37°C for 30 min. The stimulation medium was decanted from the plates, and cell lysis buffer (50 mM HEPES pH 7.2, 150 mM NaCl, 0.5% Triton X-100, 1 mM AEBSF, 10
15 KIU/ml aprotinin, 50 µM leupeptin, and 2 mM sodium orthovanadate) was added. The cells were lysed for 30 min.

In the ELISA portion of the assay, the cell lysates were added to the BSA-blocked anti-IR unit mAb (Upstate Biotechnology, Lake Placid, NY) coated ELISA plates. After a 2 hr incubation, the plates were washed 6
20 times with PBST and biotinylated anti-phosphotyrosine antibody (Upstate Biotechnology) is added. After another 2 h incubation, the plates were again washed 6 times. Streptavidin-Eu was then added, and the plates were incubated for 1 h. After washing the plates again, EG&G Wallac enhancement solution (100 mM acetone-potassium hydrogen phthalate, pH
25 3.2; 15 mM 2-naphtyltrifluoroacetate; 50 mM tri(n-octyl)-phosphine oxide; 0.1% Triton X-100) was added into each well, and the plates were placed onto a shaker for 20 min at RT. Fluorescence of samples in each well was measured at 615 nm using a VICTOR 1420 Multilabel Counter (EG&G Wallac).

30 Alternatively, IR autophosphorylation was determined using a holoenzyme phosphorylation assay. In accordance with this assay, 1 µl of purified insulin receptor (isolated from a Wheat Germ Agglutinin Expression

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System) was incubated with 25 nM insulin, or 10 or 50 μ M peptide in 50 μ l autophosphorylation buffer (50 mM HEPES pH. 8.0, 150 mM NaCl, 0.025% Triton-X-100, 5 mM MnCl_2 , 50 μ M sodium orthovanadate) containing 10 μ M ATP for 45 min at 22°C. The reaction was stopped by adding 50 μ l of gel
5 loading buffer containing β -mercaptoethanol (Bio-Rad Laboratories, Inc., Hercules, CA). The samples were run on 4-12% SDS-polyacrylamide gels. Western Blot analysis was performed by transferring the proteins onto nitrocellulose membrane. The membrane was blocked in PBS containing 3% milk overnight. The membrane was incubated with anti-phosphotyrosine
10 4G10 HRP labeled antibody (Upstate Biotechnology) for 2 h. Protein bands were visualized using SuperSignal West Dura Extended Duration Substrate Chemiluminescence Detection System (Pierce Chemical Co.).

Example 7: Fluorescence-Based HIR Binding Assays

A. Time-Resolved Fluorescence Resonance Energy Transfer Assays

15

Time-resolved fluorescence resonance energy transfer assays (TR-FRET) were used for peptide competition studies. In one set of assays, monomer and dimer peptides were tested for the ability to compete with biotinylated RP-9 monomer peptide (b-RP9) for binding to HIR-immunoglobulin heavy chain chimera (sIR-Fc; Bass *et al.*, 1996). The
20 assays were performed using a 384-well white microplate (NUNC) with a final volume of 30 μ l. Final incubation conditions were in 22 nM b-RP9, 1 nM SA-APC (streptavidin-allophycocyanin), 1 nM Eu^{3+} -sIR-Fc (LANCE™ labeled, PE Wallac, Inc.), 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl,
25 0.0027 M KCl, and 0.1 % BSA (Cohn Fraction V). After 16-24 hr of incubation at RT, the fluorescence signal at 665 nm and 620 nm was read on a Victor² 1420 plate reader (PE Wallac, Inc.). Primary data were background corrected, normalized to buffer controls, and then expressed as percent of specific binding.

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Results are shown in Figures 22A-22B. Figure 21A shows b-RP9 competition data. For these figures, the Z'-factor was greater than 0.5 ($Z' = 1 - (3\sigma_+ + 3\sigma_-) / |\mu_+ - \mu_-|$; Zhang *et al.*, 1999, *J. Biomol. Screen.* 4:67-73), and the signal-to-background (S/B) ratio was ~4-5. In Figure 22A, each data point
5 represents the average of two replicate wells. The lines represent the best fit to a four-parameter non-linear regression analysis of the data according to the following formula: $y = \min + (\max - \min) / (1 + 10^{((\log IC_{50} - x) * \text{Hillslope}))}$. This was used to determine IC_{50} values.

In another set of assays, monomer and dimer peptides were tested
10 for the ability to compete with biotinylated-S175 (b-S175) or b-RP9 for binding to sIR-Fc. The TR-FRET assays were performed in a 384-well white microplate with a final volume of 30 μ l. Final incubation conditions were in 33 nM b-S175 or 22 nM b-RP9, 1 nM SA-APC, 1 nM Eu^{3+} -sIR-Fc, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, and 0.1 % BSA.
15 After 16-24 hr of incubation at RT, the fluorescence signal at 665 nm and 620 nm was read on a Victor² 1420 plate reader. Primary data were background corrected, normalized to buffer controls, and then expressed as % Specific Binding.

Results are shown in Figures 23A-23B. For these figures, each data
20 point represents the average of two replicate wells. The lines represent the best fit to a four-parameter non-linear regression analysis of the data, which was used to determine IC_{50} values. Figure 23A shows b-S175 competition data; Figure 23B shows b-RP9 competition data.

B. Fluorescence Polarization Assays

25 Fluorescence polarization assays (FP) were used for peptide competition studies. In one set of assays monomer and dimer peptides were tested for the ability to compete with fluorescein-RP-9 (FITC-RP9) for binding to soluble HIR ectodomain (sIR; Kristensen *et al.*, 1998, *J. Biol. Chem.* 273:17780-17786). The assays were performed in a 384-well black
30 microplate (NUNC) with a final volume of 30 μ l. Final incubation conditions

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were 1 nM FITC-RP9, 10 nM sIR, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, 0.05 % BGG (bovine gamma globulin), 0.005 % Tween-20®. After 16-24 hr of incubation at RT, the fluorescence signal at 520 nm was read on an Analyst™ AD plate reader (LJL BioSystems, Inc.).

5 Primary data were background corrected using 10 nM sIR without FITC-RP9 addition, normalized to buffer controls, and then expressed as percent of specific binding. The Z'-factor was greater than 0.5 and the assay dynamic range was ~125 mP. In Figures 24-27, each data point represents the average of two replicate wells. The lines represent the best fit to a four-
10 parameter non-linear regression analysis of the data, which was used to determine IC₅₀ values. The Z'-factor was greater than 0.5 and the assay dynamic range was ~125 mP. Results are shown in Figures 24A-24B.

In another set of assays, monomer and dimer peptides were tested for the ability to compete with FITC-RP9 for binding to soluble human insulin
15 mini-receptor (mIR; Kristensen *et al.*, 1999, *J. Biol. Chem.* **274**:37351-37356). The FP assays were performed in a 384-well black microplate with a final volume of 30 µl. Final incubation conditions were 2 nM FITC-RP9, 20 nM mIR, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, 0.001 % BGG, 0.005 % Tween-20®. After 16-24 hr of incubation at RT, the
20 fluorescence signal at 520 nm was read on an Analyst™ AD plate reader. Primary data were background corrected using 20 nM mIR without FITC-RP9 addition, normalized to buffer controls and then expressed as percent of specific binding. Results are shown in Figures 25A-25B.

Monomers and dimer peptides were also tested for the ability to
25 compete with fluorescein-insulin (FITC-Insulin) for binding to sIR. The FP assays were performed in a 384-well black microplate with a final volume of 30 µl. Final incubation conditions were in 2 nM FITC-Insulin, 20 nM sIR, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, 0.05 % BGG, 0.005 % Tween-20®. After 16-24 hr of incubation at RT, the fluorescence
30 signal at 520 nm was read on an Analyst™ AD plate reader. Primary data

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were background corrected using 20 nM sIR without FITC-Insulin addition, normalized to buffer controls and then expressed as percent of specific binding. Results are shown in Figures 26A-26B.

In other assays, peptide monomers and dimer peptides were tested
5 for the ability to compete with FITC-Insulin for binding to mIR. The FP assays were performed in a 384-well black microplate with a final volume of 30 μ l. Final incubation conditions were 2 nM FITC-Insulin, 20 nM mIR, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, 0.05 % BGG (bovine gamma globulin), 0.005 % Tween-20[®]. After 16-24 hr of incubation
10 at RT, the fluorescence signal at 520 nm was read on an Analyst[™] AD plate reader. Primary data were background corrected using 20 nM mIR without FITC-RP9 addition, normalized to buffer controls and then expressed as % Specific Binding. Results are shown in Figures 27A-27B.

C. Summary

15 Table 9, below, summarizes the binding data calculated from competition assays using the IR constructs, sIR-Fc, sIR, and mIR, in TR-FRET and FP formats. The data in Table 9 indicate that most dimer peptides (e.g., S291 and S375 or S337), showed greater agonist activity than the corresponding monomer peptides (e.g., H2C or RP9, respectively)
20 in the FFC assay. It was previously demonstrated that an inequality between monomer peptides and insulin was exhibited in competition assays where the assay reporter was a monomer peptide (i.e., RP9 or S175). This inequality was also demonstrated by dimer peptides as seen in Table 9. Table 9 further shows that Group 6 monomer peptides such as E8 (D120)
25 were able to compete with FITC-RP9 or b-RP9 peptides for binding to sIR-Fc, but did not compete peptide ligands, such as FITC-RP9 for binding to mIR. Experiments using different IR constructs thereby allowed differentiation of Site I peptides based on sequence motifs (i.e., Group 6 (Formula 10) vs. Group 1 (Formula 1; A6)).

TABLE 9

	TARGET ⇒		sIR-Fc	sIR-Fc	sIR-Fc	sIR-Fc	sIR-Fc	mIR	HIR
	Label	⇒	b-S175	b-RP9	FRET	FRET	FRET	FITC-RP9	¹²⁵ I-insulin
			FRET	FRET	FRET	FRET	FRET	FP	RRA
Monomer or Dimer	SEQ ID NO:	Linkage	IC50 (nM)	Hill	IC50 (nM)	Hill	IC50 (nM)	IC50 (nM)	IC50 (nM)
H2C	2117		410	-0.82	1626	-1.03	50	-0.27	770
S291	1916 and 1917	N-N	81	-0.96	250	-0.69			1200
RP9	1558		6	-0.45	42	-0.69	10	-0.41	44
S375	1994	C-N	7	-0.80	86	-0.67			200
S337	1960 and 1961	C-C	0.2	-0.36	14	-0.57	1	-0.37	11
S391	2008		59	-0.59	610	-0.56			1500
S390	1794		27	-0.49	127	-0.49			620
S414	2015 and 2016	C-C	92	-0.62	164	-0.73			NN
S175	1560		22	-0.58	64	-0.74	10	-0.56	230
S380	2001 and 2002	C-C	10	-0.55	23	-0.64			510
E8 (D120)	2118		755	-0.74			207	-0.49	2200
Insulin			59	-0.37	63	-0.46	>100000	-0.25	0.04

FP = Time-Resolved Fluorescence Resonance Energy Transfer Assay; FP = Fluorescence Polarization Assay; RRA = Radio-Receptor Assay; FFC = Free Fat Cell Assay; N-N = N-terminal linkage; C-C = C-terminal linkage; C-N = C-terminal to N-terminal linkage; All are site 1 (formula 1) monomers or site 1-site 1 (formula 1-formula 1) dimers;

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Based on the functional studies outlined above, the following peptide dimers were designed.

SEQ ID NO:	Monom./ Linkers	Sequence
2119	F8-6aa-RP9	HLCVLEELFWGASLFGYCSGGSGGSGSLDESFYDWFERQL
2120	F8-12aa-RP9	HLCVLEELFWGASLFGYCSGGSGGSGGSGGSGSLDESFYDWFERQL
2121	D8-6aa-S175	WLDQEWAWVQCEVYGRGCPSSGGSGGSGRVDWLQRNANFYDWFVAELG
2122	D8-12aa-S175	WLDQEWAWVQCEVYGRGCPSSGGSGGSGGSGGSGRVDWLQRNANFYDWFVAELG
2123	F8-6aa-S175	HLCVLEELFWGASLFGYCSGGSGGSGRVDWLQRNANFYDWFVAELG
2124	F8-12aa-S175	HLCVLEELFWGASLFGYCSGGSGGSGGSGGSGRVDWLQRNANFYDWFVAELG
2125	D8-6aa-RP15	HLCVLEELFWGASLFGYCSGGSGGSSQAGSAFYAWFDQVLRTV
2126	D8-6aa-RP6	HLCVLEELFWGASLFGYCSGGSGGSTFYSCLASLLTGTPQPNRGPWERCRCR
2127	D8-6aa-RP17	HLCVLEELFWGASLFGYCSGGSGGSSQSDAFYSGLWALIGLSDG
2128	D8-6aa-Grp 6	HLCVLEELFWGASLFGYCSGGSGGSDSDWAGYEWFEQLD

- 5 Linker sequences are underlined and in bold; Monomer sequences are shown below; All dimers are linked C-N.

SEQ ID NO:	Monomer	Formula	Site	Sequence
1576	F8	4	2	HLCVLEELFWGASLFGYCSG
1558	RP9	1	1	GSLDESFYDWFERQL
2129	D8	6	2	WLDQEWAWVQCEVYGRGCP
1560	S175	1	1	GRVDWLQRNANFYDWFVAELG
2130	RP15	1	1	SQAGSAFYAWFDQVLRTV
1635	Rp6	2	1	TFYSCLASLLTGTPQPNRGPWERCRCR
2131	RP17	1	1	QSDAFYSGLWALIGLSDG
1595	Group 6	10	1	DSDWAGYEWFEQLD

Example 8: Peptide Fusions To The Maltose Binding Protein

10 A. Cloning

The transfer of interesting peptide sequences from phage display to maltose binding protein (MBP) fusions is desirable for several reasons. First, to obtain a more sensitive affinity estimate, the polyvalency of phage

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display peptides should be converted to a monovalent system. For this purpose, the peptide sequences are fused to MBP that generally exists as a monomer with no cysteine residues. Second, competition experiments can be carried out with the same or different peptides, one phage displayed and
5 the other fused to MBP. Lastly, purified peptides can be obtained by cleavage of the fusion protein at a site engineered in the DNA sequence.

Figure 28 shows a schematic drawing of the MBP-peptide construct. In the construct, the N-terminus of the peptide sequence is fused to the C-terminus of the MBP. Two peptide-flanking epitope tags are included, a
10 shortened-FLAG® at the N-terminus and E-Tag at the C-terminus. The corresponding gene fusion was generated by ligating a vector fragment encoding the MBP in frame with a PCR product encoding the peptide of interest. The vector fragment was obtained by digesting the plasmid pMAL-c2 (New England Biolabs) with *EcoRI* and *HindIII* and then treating the
15 fragment with shrimp alkaline phosphatase (SAP; Amersham). The digested DNA fragment was resolved on a 1% agarose gel, excised, and purified by QIAEXII (QIAGEN). The 20-amino acid peptide sequences of interest were initially encoded in the phage display vector pCANTAB5E (Pharmacia). To obtain these sequences, primers were synthesized which
20 anneal to sequences encoding the shortened FLAG® or E-Tag epitopes and also contain the required restriction enzyme sites *EcoRI* and *HindIII*. PCR products were obtained from individual phage clones and digested with restriction enzymes to yield the insert fragment. The vector and insert were ligated overnight at 15°C. The ligation product was purified using QIAquick
25 spin columns (QIAGEN) and electroporations were performed at 1500 v in an electroporation cuvette (0.1 mm gap; 0.5 ml volume) containing 10 ng of DNA and 40 µl of *E. coli* strain ER2508 (RR1 *lon::miniTn10*(Tet^r) (*malB*) (*argF-lac*)U169 Pro⁺ *zjc::Tn5*(Kan^r) *fhuA2*) electrocompetent cells (New England Biolabs). Immediately after the pulse, 1 ml of pre-warmed (40°C)
30 2xYT medium containing 2 % glucose (2xYT-G) was added and the transformants were grown at 37°C for 1 h. Cell transformants were plated

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onto 2xYT-AG plates and grown overnight at 37°C. Sequencing confirmed the clones contained the correct constructs.

B. Small-Scale Expression of Soluble MBP-Peptide Fusion Proteins

5 *E. coli* ER2508 (New England Biolabs) carrying the plasmids encoding MBP-peptide fusion proteins were grown in 2xYT-AG at 37°C overnight (250 rpm). The following day the cultures were used to inoculate media (2x YT containing-G) to achieve an OD₆₀₀ of 0.1. When the cultures reached an OD₆₀₀ of 0.6, expression was induced by the addition of IPTG to
10 a final concentration of 0.3 mM and then cells were grown for 3 h. The cells were pelleted by centrifugation and samples from total cells were analyzed by SDS-PAGE electrophoresis. The production of the correct molecular weight fusion proteins was confirmed by Western blot analysis using the monoclonal antibody anti-E-Tag-HRP conjugate (Pharmacia).

C. Large-Scale Expression of Soluble MBP-Peptide Fusion Proteins

E. coli ER2508 carrying plasmids encoding the MBP-peptide fusion proteins were grown in 2xYT-AG media for 8 h (250 rpm, 37°C). The cultures were subcultured in 2xYT-AG to achieve an OD₆₀₀ of 0.1 and grown
20 at 30°C overnight. This culture was used to inoculate a fermentor with medium of following composition (g/l): glucose (3.00); (NH₄)₂SO₄ 5.00; MgSO₄ • 7H₂O (0.25); KH₂PO₄ (3.00); citric acid (3.00); peptone (10.00); and yeast extract (5.00); pH 6.8.

 The culture was grown at 700 rpm, 37°C until the glucose from the
25 medium was consumed (OD₆₀₀ = ~6.0 – 7.0). Expression of the fusion protein was induced by the addition of 0.3 mM IPTG and the culture was grown for 2 h in fed-batch mode fermentation with feeding by 50 % glucose at a constant rate of 2 g/l/h. The cells were removed from the medium by centrifugation. Samples of the cell pellet were analyzed by SDS-PAGE

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followed by the Western blot analysis using the mouse monoclonal antibody anti-E-Tag-HRP conjugate (Pharmacia) to visualize the expressed product.

D. Purification

The cell pellets were disrupted mechanically by sonication or
5 chemically by treatment with the mild detergent Triton X-100. After removal
of cell debris by centrifugation, the soluble proteins were prepared for
chromatographic purification by dilution or dialysis into the appropriate
starting buffer. The MBP fusions were initially purified either by amylose
affinity chromatography or by anion exchange chromatography. Final
10 purification was performed using anti-E-Tag antibody affinity columns
(Pharmacia). The affinity resin was equilibrated in TBS (0.025 M Tris-
buffered saline, pH 7.4) and the bound protein was eluted with Elution buffer
(100 mM glycine, pH 3.0). The purified proteins were analyzed for purity
and integrity by SDS-PAGE and Western blot analysis according to standard
15 protocols.

For MBP fusions, IR agonist activity was observed for the Site 1-Site
1 dimer peptides shown in Table 10, below. Additional binding data for the
MBP fusions are shown in Table 11, also below.

TABLE 10

Fus.	Monomer/ Linker	Sequence	SEQ ID NO.	Form.	Act.	Site IR	Fus. Conc.	MW (kDa)	K _d (HIR)
426	D8	MBP...NNNNLIEGRISIEFIEGR AQPAMA WLDQEWAWVQCEVYGRGCPAAAA (ETAG)AA	2132	6	N	2	0.76	52.2	1.4 x 10 ⁻⁶
429	D8-6aa-D8	MBP...NNNNLIEGRISIEFIEGRAQPAMAWLDQEWAWVQCEVYGRGCPGGSGGS KWLDQEWAWVQCEVYGRGCPAAAA(ETAG)AA	2133	6-6	N-N	2-2	3.2	55.3	1.3 x 10 ⁻⁶
430	H2C-4aa-RB6	MBP...NNNNLIEGRISIEFIEGRDYKDDDKFHENFYDFVQRQVSGSLDALDRLM RYFEERPSLETAG	2134	1-6	A-	1-1	0.17	54.5	2.1 x 10 ⁻⁶
431	H2C-6aa-F8	MBP...NNNNLIEGRISIEFIEGRDYKDDDKFHENFYDFVQRQVSGSGSHLCVLEE LFWGASLFGYCSGAAA(ETAG)AA	2135	1-4	A-N	1-2	3.3	54.8	4.7 x 10 ⁻⁸
432	H2C-12aa-F8	MBP...NNNNLIEGRISIEFIEGRDYKDDDKFHENFYDFVQRQVSGSGSGSGGS HLCVLEELFWGASLFGYCSGAAA(ETAG)AA	2136	1-4	A-N	1-2	2.9	55.5	3.5 x 10 ⁻⁸
433	H2C-9aa-F8	MBP...NNNNLIEGRISIEFIEGRDYKDDDKFHENFYDFVQRQVSGSGSGSGSHLC VLEELFWGASLFGYCSGAAA(ETAG)AA	2137	1-4	A-N	1-2	2.8	55.2	2.1 x 10 ⁻⁸
434	G3-12aa-G3	MBP...NNNNLIEGRISIEFIEVRAQPAMARGGGTFYEFWESALRKHGAGGGSGSG SGSGRGGGTFYEFWESALRKHGAGAAA(ETAG)AA	2138	1-1	N-N	1-1	0.01	56	3.2 x 10 ⁻⁶
436	H2C-9aa-H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMAFHENFYDFVQRQVSGSGSGSGSFHEN FYDFVQRQVSA(ETAG)AA	2139	1-1	A	1-1	1.1	54.2	4.1 x 10 ⁻⁷
437	H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMA FHENFYDFVQRQVSA(ETAG)AA	2140	1	N-N	1	0.3	51.5	8.3 x 10 ⁻⁶
427	G3-6aa-G3	MBP...NNNNLIEGRISIEFIEGRAQPAMARGGGTFYEFWESALRKHGAGGGSGSR GGGTFYEFWESALRKHGAGAAA(ETAG)AA	2141	1-1	N-N	1-1	0.02	55.3	3.3 x 10 ⁻⁶
435	H2C-3aa-H2C- 3aa-H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMAFHENFYDFVQRQVSGSGSFHENFYDFV RQVSGSGSFHENFYDFVQRQVSA(ETAG)AA	2142	1-1-1	A-A-A	1-1- 1	2.1	55.5	2.0 x 10 ⁻⁶
439	H2C-6aa-H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMAFHENFYDFVQRQVSGSGSGSFHEN FYDFVQRQVSA(ETAG)AA	2143	1-1	A-A	1-1	1.4	53.9	5.5 x 10 ⁻⁷
449	H2C-12aa-H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMAFHENFYDFVQRQVSGSGSGSGSGSA QPAMAFHENFYDFVQRQVSA(ETAG)AA	2144	1-1		1-1	1.5	51.8	6.2 x 10 ⁻⁷
452	G3	MBP...NNNNLIEGRISIEFIEGRAQPAMARGGGTFYEFWESALRKHGAGAA A(ETAG)AA	2145	1		1	0.15	48.8	7.8 x 10 ⁻⁷
463	H2C-3aa-H2C	MBP...NNNNLIEGRISIEFIEGRAQPAMAFHENFYDFVQRQVSGSGSFHENFYDFV RQVSA(ETAG)AA	2146	1-1	A-A	1-1	1.8	50.1	9.6 x 10 ⁻⁷

464	LF-H2C	MBP...NNNNLGI ^{RISE} FI ^{GRDY} KDDDDK FHENFYDWFVRQVSAA(ETAG)AA	2147	1		1	0.045	48.4	3.9 x 10 ⁻⁸
446	LF-F8	MBP...NNNNLGI ^{RISE} FI ^{GRDY} KDDDDKHL ^{CVLEEL} FWGASLFGYCSGAAA(ETA GJAA	2148	1		2	1.9	49.1	7.7 x 10 ⁻⁷
459	SF-RB6	MBP...NNNNLGI ^{RISE} FI ^{GSADY} KDL ^{DAL} RLMRYFEERPSLAAA(ETAG)AA	2149	3		1	0.069	48.1	7.7 x 10 ⁻⁸
MB P*	lacZ	**		na			5.1	50	> 1 x 10 ⁻⁵

*MBP (negative control for the fusions) is fused to a small fragment of beta-galactosidase (lacZ); **MBP-lacZ fusion protein was derived from the plasmid pMal-c2 as purchased from NEB. Fus. = fusion; Act. = activity; Conc. = concentration; N = Antagonist; A = Agonist; LF = Long FLAG® epitope (DYKDDDDK; SEQ ID NO:1777); SF = Short FLAG® epitope (DYKD; SEQ ID NO:1545); na = not applicable; Form. = formula; All dimers are linked C-N; Linker sequences are underlined.

TABLE 11

Fusion	Monomer/ Linker	Sequence	SEQ ID NO.	Form.	Site IR	High conc. tested (μM)	Kd (HIR) μM
431-	H2C-6aa-F8	MBP...NNNNLGI ^{RISE} FI ^{GRDY} KDDDKFHENFYDWFVRQVSGGGSHLCVLEELFWGASLFGYCS GAAA(ETAG)AA	2150	1-6	1-2	0.2	0.033
431+	H2C-6aa-F8	DYKDDDKFHENFYDWFVRQVSGGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	2151	1-6	1-2	0.2	0.0074
432-	H2C-12aa-F8	MBP...NNNNLGI ^{RISE} FI ^{GRDY} KDDDKFHENFYDWFVRQVSGGGGGSHLCVLEELFWGA SLFGYCSGAAA(ETAG)AA	2152	1-6	1-2	0.2	0.02
432+	H2C-12aa-F8	DYKDDDKFHENFYDWFVRQVSGGGGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	2153	1-6	1-2	0.2	0.0038
433-	H2C-9aa-F8	MBP...NNNNLGI ^{RISE} FI ^{GRDY} KDDDKFHENFYDWFVRQVSGGGGGSHLCVLEELFWGASLFG YCSGAAA(ETAG)AA	2154	1-6	1-2	0.2	0.03
433+	H2C-9aa-F8	DYKDDDK FHENFYDWFVRQVSGGGGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	2155	1-6	1-2	0.2	0.004

The concentrations of these fusions vary depending on the expression quality. There are 2 sets of each fusion: uncleaved (-) and cleaved with factor Xa (+). The fusion proteins are in Tris buffer (20 mM Tris, 200 mM NaCl, 1 mM EDTA, 50 mM maltose, pH 7.5) and the cleaved fusions (+) are in the same Tris buffer (500 μl) + 12 μg Factor Xa. (Source of Factor Xa: New England Biolabs). Conc. = concentration; Form. = formula; All dimers are linked C-N; Linker sequences are underlined.

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E. BIAcore Analysis

For BIAcore analysis of fusion protein and synthetic peptide binding to insulin receptor, insulin (50 µg/ml in 10 mM sodium acetate buffer pH 5) was immobilized on the CM5 sensor chip (Flowcell-2) by amine coupling. Flowcell-1 was used for background binding to correct for any non-specific binding. Insulin receptor (450 nM) was injected into the flow cell and the binding of IR to insulin was measured in resonance units (RUs). Receptor bound to insulin gave a reading of 220 RU. The surface was regenerated with 25 mM NaOH. Pre-incubation of receptor with insulin in a tube at RT completely abrogated the response units to 16 RU. Thus, the system was validated for competition studies. Several maltose-binding fusion proteins, peptides, and rVabs were pre-incubated with insulin receptor before injecting over the insulin chip for competition studies. The decrease in binding/resonance units indicates that several MBP-fusion proteins can block the insulin-binding site. The results are shown in Tables 12 and 13. The amino acid sequences referred to in the tables are identified in Figures 8 and 9A-9B, except the 447 and 2A9 sequences, which are shown below.

TABLE 12

BIAcore Results—Fusion Proteins Compete for Binding to IR

	Incubation Mixtures	Result (RUs)	Sequence Type
Controls	Insulin Receptor (IR) 450 nM	220	Positive Control
	Insulin (8.7 µM)	16	Negative Control
MBP Fus. Prots.	A7 (20A4)-MBP (4.1 µM) + IR	43	Formula 6 Motif
	D8-MBP (1.6 µM) + IR	56	Formula 6 Motif
	D10-MBP (3.4 µM) + IR	81	Formula 11 Motif
	447-MBP (11.5 µM) + IR	195	hGH Pept. Fus.
	MBP (13 µM) + IR	209	Negative Control

The A7 (20A4), D8, and D10 peptide sequence are shown in Figures 8 and 9A-9B. The 447 peptide sequence is: LCQRLGVGWPGWLSGWCA (SEQ ID NO:2156).

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TABLE 13

BIAcore Results -- Synthetic peptides compete for binding to IR

Incubation Mix	% Binding	Result (RUs)	Sequence Type
IR	100	128	Positive control
IR + 20D1	41	51.8	Formula 1 Motif
IR + D8	33	41.6	Formula 6 Motif
IR + 20C11	38	49	Formula 2 Motif (bkg high)
IR + H2	27	34.6	IGF (phosphorylated band)
IR + 2A9	100	128	IGF(bkg high)
IR + 20A4	33	41.8	Formula 6 Motif
IR + p53wt	97	124.5	P53 wild type

5 The concentration of each peptide was about 40 μ M and the concentration of IR was 450 nM. The 20D1, 20A4, and D8 peptide sequences are shown in Figures 8 and 9A-9B. The remaining peptide sequences are as follows: 447 = LCQRLGVGWPGWLSGWCA (SEQ ID NO:2156); 2A9 = LCQSWGVRIGWLTGLCP (SEQ ID NO:2157); 20C11 = DRAFYNGLRDLVGAVYGAWD (SEQ ID NO:1659); H2 = VTFTSAVFHENFYDWFVRQVS (SEQ ID NO:1784).

10

Regarding preparation of a Site 1 agonist comprising two D117 (H2C) peptides, a linker of only 3 amino acids (12 Å) provided a ligand of greater affinity for Site 1 of IR than a corresponding ligand prepared with a 9 amino acid (36 Å) linking region (Figure 29).

15 F. Stimulation of Autophosphorylation of IR by MBP-Fusion Peptides

MBP fusion peptides were prepared as described above, and then assayed for autophosphorylation of a insulin receptor construct transfected into 32D cells (Wang *et al.*, 1993; clone 969) (see Example, above). The results of these experiments shown in Figure 30 indicate that the H2C monomer and H2C-H2C homodimer peptides stimulate autophosphorylation of IR *in vivo*. H2C dimer peptides (Site 1-Site 1) with a 6 amino acid linker (H2C-6aa-H2C) were most active in the autophosphorylation assay. Other active dimer peptides are also shown in Figure 30, particularly H2C-9aa-H2C, H2C-12aa-H2C, H2C-3aa-H2C, and F8.

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G. Insulin Receptor Binding Affinity and Fat Cell Potency of MBP-Fusion Peptides

Results of assays to determine binding affinity for insulin receptor and fat cell potency of the MBP-fusion peptides are shown in Table 14, below.

TABLE 14

Peptide	SEQ ID NO:	Formula	Site IR	Sequence	HIR Kd (mol/l)	FFC
RB426	2158	F6	2	MBP...NNNNGIEGRISIEFIEGR AQPAMA WLDQEWAWVQCEVYGRGCPs AAA(ETAG)AA	1.4*10 ⁻⁶	
RB429	2159	F6-F6	2-2	MBP...NNNNGIEGRISIEFIEGR AQPAMAWLDQEWAWVQCEVYGRGCPsGGGSKWLDQEWAWVQCEVYGRGCPsAAA(ETAG)AA	1.3*10 ⁻⁶	
RB505M	2160	F4	2	MBP...NNNNGIEGRISIEFIEGRDYKDDDK HLCVLEELFWGASLFYCSGAAA(ETAG)AA		
RB517M	2161	F4-F4	2-2	MBP...NNNNGIEGRISIEFIEGRDYKDDDK HLCVLEELFWGASLFYCSGAAA(ETAG)AA		
RB515	2162	F4-F4	2-2	MBP...NNNNGIEGRISIEFIEGRDYKDDDK HLCVLEELFWGASLFYCSGAAA(ETAG)AA HLCVLEELFWGASLFYCSGAAA(ETAG)AA		
RB510	2163	F4-F4-F4	2-2-2	MBP...NNNNGIEGRISIEFIEGRDYKDDDK HLCVLEELFWGASLFYCSGAAA(ETAG)AA HLCVLEELFWGASLFYCSGAAA(ETAG)AA		
RB437	2164	F1	1	MBP...NNNNGIEGRISIEFIEGR AQPAMA FHENFYDWFVRQVSA(ETAG)AA	8.3*10 ⁻⁶	
RB463	2165	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMAFHNFYDWFVRQVSA(ETAG)AA	9.6*10 ⁻⁷	
RB439	2166	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMA FHENFYDWFVRQVSA(ETAG)AA	5.5*10 ⁻⁷	
RB436	2167	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMAFHNFYDWFVRQVSA(ETAG)AA	4.1*10 ⁻⁷	
RB449	2168	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMAFHNFYDWFVRQVSA(ETAG)AA	6.2*10 ⁻⁷	
RB435	2169	F1-F1-F1	1-1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMAFHNFYDWFVRQVSA(ETAG)AA	2.0*10 ⁻⁶	
RB502	2170	F1	1	MBP...NNNNGIEGRISIEFIEGRDYKDDDK VRVDWLQRNANFYDWFVAEL VAAA(ETAG)AA		
RB508M	2171	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGRDYKDDDK VRVDWLQRNANFYDWFVAELGGGSGRVDWLQRNANFYDWFVAELGAAA(ETAG)AA		
RB509M	2172	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGRDYKDDDK VRVDWLQRNANFYDWFVAELGGGSGRVDWLQRNANFYDWFVAELGAA A(ETAG)AA		
RB452	2173	F1	1	MBP...NNNNGIEGRISIEFIEGR AQPAMARGGTFYEFESALRKHGAGAAA(ETAG)AA	7.8*10 ⁻⁷	
RB427	2174	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMARGGTFYEFESALRKHGAGGSGRGGTFYEFESALRKHGAGAAA(ETAG)AA	3.3*10 ⁻⁶	
RB434	2175	F1-F1	1-1	MBP...NNNNGIEGRISIEFIEGR AQPAMA RGGGTFYEFESALRKHGAGGSGRGGTFYEFESALRKHGAGAAA(ETAG)AA	3.2*10 ⁻⁶	

RB513	2176	F1	1	MBP ..NNNLLGIEGRISFIEGRDYKDDDDKGSLSDFYDWFERQLGKAAA(ETAG)AA	
RB516	2177	F1-F1	1-1	MBP...NNNLLGIEGRISFIEGRDYKDDDDKGSLSDFYDWFERQLGKGGSGGSLDESFDYDWFERQLGKAAA(ETAG)AA	
RB512	2178	F1-F1	1-1	MBP ...NNNLLGIEGRISFIEGRDYKDDDDKGSLSDFYDWFERQLGKGGSGGSLDESFDYDWFERQLGKAAA(ETAG)AA	
RB464	2179	F1	1	MBP ..NNNLLGIEGRISFIEGRDYKDDDDKHLVLEELFWGASLFGYCSGAAA(ETAG)AA	3.8*10 ⁻¹⁸
RB446	2180	F4	2	MBP ..NNNLLGIEGRISFIEGRDYKDDDDKHLVLEELFWGASLFGYCSGAAA(ETAG)AA	7.7*10 ⁻⁷
RB459	2181	F3	1	MBP ..NNNLLGIEGRISFIEGSDYKDLDALDRLMRYFEERPSLAAA(ETAG)AA	7.7*10 ⁻⁸
RB430	2182	F1-F3	1-1	MBP...NNNLLGIEGRISFIEGRDYKDDDDKHFENFYDWFVRQVSGSGGS LDALDRLMRYFEERPSLETAG	2.1*10 ⁻⁶
RB430	2183	F1-F3	1-1	cleaved DYKDDDKHFENFYDWFVRQVSGSGSLDALDRLMRYFEERPSLAAA(ETAG)AA	~4*10 ⁻⁹
RB431	2184	F1-F4	1-2	MBP...NNNLLGIEGRISFIEGRDYKDDDKHFENFYDWFVRQVSGSGGS HLCVLEELFWGASLFGYCSGAAA(ETAG)AA	4.7*10 ⁻⁸
RB431	2185	F1-F4	1-2	cleaved DYKDDDKHFENFYDWFVRQVSGSGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	~8*10 ⁻⁹
RB432	2186	F1-F4	1-2	MBP...NNNLLGIEGRISFIEGRDYKDDDKHFENFYDWFVRQVSGSGSGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	3.5*10 ⁻⁸
RB432	2187	F1-F4	1-2	cleaved DYKDDDKHFENFYDWFVRQVSGSGSGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	~6*10 ⁻⁹
RB433	2188	F1-F4	1-2	MBP...NNNLLGIEGRISFIEGRDYKDDDK HFENFYDWFVRQVSGSGSGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	2.1*10 ⁻⁸
RB508	2189	F1-F1	1-1	DYKDDDDKVRVWDLQRNANFYDWFVAELGGSGSGRVDWLQRNANFYDWFVAELGAAAGAPVYPDPLEPRSA	1.5*10 ⁻⁷
RB509	2190	F1-F1	1-1	DYKDDDDKVRVWDLQRNANFYDWFVAELGGSGSGGSGRVDWLQRNANFYDWFVAELGAAAGAPVYPDPLEPRAA	5.5*10 ⁻⁸
RB505	2191	F4	2	DYKDDDDKHLVLEELFWGASLFGYCSGAAA(ETAG)AA	4.8*10 ⁻⁷
RB517	2192	F4-F4	2-2	DYKDDDDKHLVLEELFWGASLFGYCSGSGGSHLCVLEELFWGASLFGYCSGAAA(ETAG)AA	6.0*10 ⁻⁶
RB521	2193	F1-F1	1-1	MADYKDDDDKGSLSDFYDWFERQLGKGGSGGSLDESFDYDWFERQLGKAAA(ETAG)PG	4.4*10 ⁻⁸
RB535	2194	F1-F1	1-1	MADYKDDDDKGSLSDFYDWFERQLGKGGSGGSGGSLDESFDYDWFERQLGKAAA(ETAG)PG	~1.0*10 ⁻⁷
RB540	2195	F6	2	MADYKDDDDKWLQDEWAWVQCEVYGRGCPSSAA(ETAG)PG	~1.0*10 ⁻⁷
RB539	2196	F6-F1	2-1	MADYKDDDDKWLQDEWAWVQCEVYGRGCPSSGSGGSLDESFDYDWFERQLGKAAA(ETAG)PG	7*10 ⁻¹⁰
RB537	2197	F1-F6	1-2	MADYKDDDDKGSLSDFYDWFERQLGKGGSGGSLQDEWAWVQCEVYGRGCPSSAA(ETAG)PG	5.9*10 ⁻¹¹
RB538	2198	F1-F6	1-2	MADYKDDDDKGSLSDFYDWFERQLGKGGSGGSGGSLQDEWAWVQCEVYGRGCPSSAA(ETAG)PG	1.7*10 ⁻¹¹
RB626	2199	F6-F1	2-1	MADYKDEIAEWGRVRLVYGRVCGGSGGSGGSLDESFDYDWFERQLGKAAA(ETAG)PG	3.0*10 ⁻¹⁰

RB625	2200	F6-F1	2-1	MADYKDDDDKWLDQEWAWVQCEVYGRGCPSPPPPDITTHRADPQGSLSDESFYDWFERQLGKAAA(ETAG)PG	3.8×10^{-10}	++++
RB622	2201	F6-F1	2-1	MADYKDDDDKWLDQEWAWVQCEVYGRGCPSTPKPTPPPLSADGSLDESFYDWFERQLGKAAA(ETAG)PG	1.0×10^{-9}	++++
RB596	2202	F1	1	MQNDDGSLDESFYDWFERQLGHHHHHPG	9.4×10^{-8}	
RB569	2203	F1	1	MGSLSDESFYDWFERQLGEEEGDHHHHHPG	2.1×10^{-7}	
RB570	2204	F1	1	MQNDDGSLDESFYDWFERQLGEEEGDHHHHHPG	2.5×10^{-8}	

ETAG = GAPVYPDPLEPR(SEQ ID NO: 2205); MBP...NINNL = fusion junction to MBP at c-terminus of MBP; All dimers are linked C-N.

Example 9: *In Vivo* Assays for Insulin Agonists

To test the *in vivo* activity of dimer peptide S519, an intravenous blood glucose test was carried out on Wistar rats. Male Mol:Wistar rats, weighing about 300 g, were divided into two groups. A 10 µl sample of
5 blood was taken from the tail vein for determination of blood glucose concentration. The rats were anaesthetized with Hypnorm/Dormicum at t = -30 min and blood glucose was measured again at t = -20 min and at t = 0 min. After the t = 0 sample was taken, the rats were injected into the tail vein with vehicle or test substance in an isotonic aqueous buffer at a
10 concentration corresponding to a 1 ml/kg volume of injection. Blood glucose was measured at times 10, 20, 30, 40, 60, 80, 120, and 180 min. The Hypnorm/Dormicum administration was repeated at 20 minute intervals. Results shown in Figure 33 demonstrate that the S519 (at 20 nmol/kg) peptide lowered blood glucose levels similar to levels observed for human
15 insulin (at 2.5 nmol/kg) (n=8). The S519 peptide and human insulin showed comparable *in vivo* effects, both in magnitude and onset of response (Figure 33).

Example 10: IGF-1 Surrogates

Three major groups of peptide IGF-1 surrogates were obtained from
20 IGF-1R panning experiments: Site 1 A6 (FyxWF) (SEQ ID NO: 1596); Site 1 B6 (FyxxLxxL) (SEQ ID NO: 1732), and Site 2 (C-C looped). See Beasley *et al.* International Application PCT/US00/08528, filed March 29, 2000, and Beasley *et al.*, U.S. Application Serial No. 09/538,038, filed March 29, 2000. Active surrogates included 20E2 and RP6 (B6-like; Formula 2), S175 (A6-
25 like; Formula 1), G33 (A6-like; Formula 1), RP9 (A6-like; Formula 1), D815 (Site 2), and D8B12 (Site 2) peptides. The IGF-1 surrogates were analyzed by various assays, described as follows.

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A. Phage Competition

Phage competition studies were performed with Site 1 (RP9) and Site 2 (D815) monomer peptides. Plates were coated with IGF-1R (100 ng/well in carbonate buffer, pH 9.6) overnight at 4°C. Wells were blocked with 4% non-fat milk in PBS for 60 min at room temperature. One hundred microliters of rescued phage were added to each well. Peptides in varying concentrations were added and the mixtures were incubated for 2 hr at room temperature. Plates were washed three times with PBS and 100 µl of anti-M13 antibody conjugated to horseradish peroxidase was added to each well. The labeled antibody was incubated at room temperature for 60 min. After washing, 100 µl of ABTS was added per well and the plates read in a microtiter reader at 450 nM.

Phage included RP9 (A6-like; Formula 1); RP6 (B6-like; Formula 2); D8B12 (Site 2); and D815 (Site 2). Peptides included RP9 and D815.

15

Peptide	Formula	Site IGF-1R	Sequence	SEQ ID NO:
D8B12	6	2	WLEQERAWIWCEIQGSGCRA	1884
D815	6	2	WLDQERAWLWCEISGRGCLS	2206
RP6	2	1	TFYSCLASLLTGTPQPNRGPWERCRCR	1635
RP9	1	1	GSLDESFYDWFERQLG	1559

Results shown in Figures 34A-34E demonstrate that that RP9 and D815 peptides competed both Site 1 and Site 2 phage. These results illustrate the allosteric nature of the interaction with IGF-1R.

Phage competition studies were also performed with Site 2-Site 1 dimer peptides containing 6- or 12-amino acid linkers. Plates were coated with IGF-1R (100 ng/well in carbonate buffer, pH 9.6) overnight at 4°C. Wells were blocked with 4% non-fat milk in PBS for 60 min at room temperature. One hundred microliters of rescued phage were added to each well. Peptides in varying concentrations were added and the mixture

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incubated for 2 hr at room temperature. Plates were washed three times with PBS and 100 μ l of anti-M13 antibody conjugated to horseradish peroxidase was added to each well. The labeled antibody was incubated for 60 min at room temperature. After washing, 100 μ l of ABTS was added per well and the plates read in a microtiter reader at 450 nM. Phage included RP9, RP6, D8B12, and D815. Peptides included D815-6L-RP9 and D815-12L-RP9. Linker sequences are underlined and shown below.

Peptide	Formula	Site IGF-1R	Sequence	SEQ ID NO:
D815-6L-RP9	6-1	2-1	LDQERAWLWCEISGRGCLSGGSGGSGSLDESFYDWFERQLGK K	2207
D815-12L-RP9	6-1	2-1	WLDQERAWLWCEISGRGCLSGGSGGSGGSGGSGSLDESFYD WFERQLGKK	2208

D8B12, D815, RP6, and RP9 amino acid sequences are shown in the previous section. Results shown in Figures 35A-35E demonstrate that dimers competed both Site 1 and Site 2 phage. This indicates that both dimer units were active at IGF-1R.

B. IGF-1 Proliferation Assays

FDCEP-2 cells expressing the IL-3 and human IGF-1R receptors were grown in RPMI-1640 medium supplemented with 15% fetal bovine serum (FBS) and 5% WEHI conditioned medium (containing IL-3) in accordance with routine methods. Prior to an experiment, the cells were pelleted and washed two times in PBS. Following this, cells were resuspended in RPMI-1640 medium with 2% FBS and added to a 96-well plate at a concentration of 2×10^4 cells/well in 75 μ l. This was designated as the cell plate.

Peptides were suspended in PPMI-15% FBS (test medium). For the agonist assay, medium was added to rows 2-12 of a 96 well plate. The peptide was added to row 1 in 200 μ l of test medium at a final concentration of 60 μ M. The peptide was serially diluted (1:1) across rows 2-11. No peptide was added to row 12 (control; cells without IGF-1). For the

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antagonist assay, test medium containing 10 ng/ml IGF-1 (ED₅₀ test medium) was added to all wells of a 96 well plate. To row 1 was added 100 μ l of peptide in ED₅₀ test medium at a concentration of 120 μ M. The peptide was serially diluted (1:1) across rows 2-11. No peptide was added to row 12 (control; cells with IGF-1).

For both agonist and antagonist assays, 75 μ l from the working plates was transferred to the appropriate rows in comparable cell plates. The starting peptide concentration for both agonist and antagonist assays was 30 μ M. Each peptide was done in duplicate. Plates were incubated at 37°C for 45-48 hr. Ten microliters of WST-1 (Cell Proliferation Reagent, Roche cat # 1 644 807) were added to each well and the plates were read in an ELISA reader (440/700 dual wavelength) each hour for 4 hr. Graphs were prepared from the raw data using Sigma Plot. Peptides included:

Peptide	Formula	Site IGF-1R	Sequence	SEQ ID NO:
20E2	2	1	DYKDFYDAIDQLVRGSARAGGTRD	2209
D815	6	2	WLDQERAWLWCEISGRGCLS	2206
G33	1	1	GIISQSCPESFYDWFAGQVSDPWWCW	1600
RP6	2	1	TFYSCLASLLTGTPQPNRGPWERCRCR	1635
RP9	1	1	GSLDESFYDWFERQLG	1559
S175	1	1	GRVDWLQRNANFYDWFVAELG	1560

15

Results of the IGF-1 proliferation assays are shown in Figures 36-42. Figure 36 demonstrates that that peptides G33 (Site 1; ED₅₀ ~ 10 μ M) and D815 (Site 2; ED₅₀ ~ 2 μ M) showed agonist activity at IGF-1R, whereas peptides RP9 and RP6 showed no agonist activity. Figure 37 demonstrates that that peptides RP6 (Site 1; ED₅₀ ~ 1 μ M) and RP9 (Site 1; ED₅₀ ~ 7 μ M) showed antagonist activity at IGF-1R, whereas peptides G33 and D815 showed no antagonist activity. Figure 38 demonstrates that peptides S175 and 20E2 exhibited weak agonist activity at IGF-1R (ED₅₀ > 10 μ M). Figure

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39 shows that D815-RP9 dimers with 6- or 12-amino acid linkers acted as agonists at IGF-1R. Figure 40 shows that dimer peptide D815-6-G33 was inactive as an agonist at IGF-1R. Figure 41 shows that monomer peptide RP6 acted as an antagonist at IGF-1R. The IGF-1 standard curve
5 determined for FDCP-2 cells is shown in Figure 42.

The IGF-1R data for the Site 1 and Site 2 peptides is summarized in Table 15, below.

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TABLE 15

Mon./Dimer	Form.	Site IGF-1R	Link.	Sequence	SEQ ID NO:	nM Ki app Kd	nM ED ₅₀ Growth	Max Action	nM IC ₅₀ Antag.	Ki/ ED ₅₀	Class
IGF-1			NA			0.69	0.30	100	2	2.3	A
rG33	1	1	NA	GIISQSCPESFYDWFAGQVSDPWWCW	1600	1450	500	>50	---	2.9	A
rD815	6	2	NA	WLDQERAWLWCEISGRGCLS	2206	4080	500	>50%	---	8.2	A
RP9	1	1	NA	GSLDESFYDWFERQLG	1559	417	---	<10%	900	0.5	N
D815-G33	6-1	2-1	6 aa	WLDQERAWLWCEISGRGCLSGGGGGSGGIISQSCPESF YDWFAGQVSDPWWCW	2210	624	---	<10%	nd		nd
D815-RP9	6-1	2-1	6 aa	WLDQERAWLWCEISGRGCLSGGGGGSGGSLDESFYDW FERQLGKK	2211	36	50	>50%	>500	0.8	A
D815-RP9	6-1	2-1	12 aa	WLDQERAWLWCEISGRGCLSGGGGGSGGGSGSL DESFYDWFERQLGKK	2212	3	10,000	100	----	0.0003	A

A = agonists; N = antagonist; nd = not determined; NA = not applicable; Form. = formula; Mon. = monomer; Antag. = antagonist; Link. = linker; Linker sequences are underlined.

Example 11: Panning Peptide Libraries

A. Panning IGF-1 Surrogate Secondary Libraries

Soluble IGF-1R ("sIGF-1R") was obtained from R&D Systems. The soluble protein (> 95% pure) included the heterotetrameric (alpha 2-beta 2) extracellular domain of IGF-1R isolated from a mouse myeloma cell line. sIGF-1R (500 ng/well) was added to an appropriate number of wells in a 96-well microtiter plate (MaxiSorp plates, NUNC) and incubated overnight at 4°C. Wells were then blocked with MPBS (PBS buffer pH 7.5 containing 2% Carnation® non-fat dry milk) at room temperature (RT) for 1 h. Eight wells were used for each round of panning for the G33 and RP6 secondary libraries. The phage were incubated with MPBS for 30 min at RT, then 100 µl was added to each well.

For the first round, the input phage titer was 4×10^{13} cfu/ml. For rounds 2 and 3, the input phage titer was approximately 10^{11} cfu/ml. Phage were allowed to bind for 2 to 3 h at RT. The wells were then quickly washed 13 times with 200 µl/well of MPBS. Bound phage were eluted by incubation with 100 µl/well of 20 mM glycine-HCl, pH 2.2 for 30 s. The resulting solution was then neutralized with Tris-HCl, pH 8.0. Log phase TG1 cells were infected with the eluted phage, then plated onto two 24 cm x 24 cm plates containing 2xYT-AG. The plates were incubated at 30° C overnight. The next morning, cells were removed by scraping and stored in 10% glycerol at -80° C. For subsequent rounds of affinity enrichment, cells from these frozen stocks were grown and phage were prepared as described above. A minimum of 72 clones was picked at random from the second, third, and fourth rounds of panning and screened for binding activity. DNA sequencing of the clones determined the amino acid sequences summarized in Figure 43A-43B.

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B. Panning Peptide Dimer Libraries

Microtiter plates were coated and blocked by standard methods, as follows. Plates were coated with sIGF-1R (see Example, above) or soluble IR (Bass construct; Bass *et al.*, 1996, *J. Biol. Chem.* **271**:19367-19375) in
5 0.2 M NaHCO₃, pH 9.4. One hundred microliters of solution containing either 50 ng IR or IGF-1R (rounds 1 and 2), 25 ng IR or IGF-1R (round 3), or 12.5 ng IR or IGF-1R (round 4) was added to an appropriate number of wells in a 96-well microtiter plate (MaxiSorp plates, Nalge NUNC) and incubated overnight at 4°C. Wells were then blocked with a solution of 2%
10 non-fat milk in PBS (MPBS) at RT for at least 1 h.

Eight wells coated with IR or IGF-1R were used for each round of panning. One hundred microliters of phage were added to each well. For the first round, the input phage titer was 3×10^{13} cfu/ml. For subsequent rounds, the input phage titer was approximately 10^{12} cfu/ml. Phage were
15 incubated for 2-3 h at RT. The wells were then quickly washed 13 times with 300 μ l/well of PBS. Bound phage were eluted by incubation with 150 μ l/well of 50 mM glycine-HCl, pH 2.0 for 15 min. The resulting solution was pooled and then neutralized with Tris-HCl, pH 8.0. Log phase TG1 cells were infected with the eluted phage, in 2xYT medium for 1 hr at 37°C prior
20 to the addition of helper phage, ampicillin, and glucose (2% final concentration).

After incubation for 1 hr at 37°C, the cells were spun down and resuspended in 2xYT-AK medium. The cells were then returned to the shaker and incubated overnight at 37°C. Phage amplified overnight were
25 then precipitated and subjected to the next round of panning. A total of 96 clones were picked at random from rounds 3 and 4 and screened for binding activity. Several clones from each pan were further tested for binding to IR or IGF-1R in phage ELISA by competition with soluble peptides as described in Beasley *et al.* International Application PCT/US00/08528, filed
30 March 29, 2000, and Beasley *et al.*, U.S. Application Serial No. 09/538,038, filed March 29, 2000. Competition was performed by addition of 5 μ l of RP9

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peptide, recombinant D8 peptide, or both per well, followed by addition of 100 μ l of phage per well. Representative peptides are shown in Figures 44A-44B and in Table 16, below.

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TABLE 16

Pep.	SEQ ID NO:	Form.	Site IR	Sequence	Description
RP27	2213	6-1	2-1	GLDQEQAWVECEVYGRGCPYGSLSDESFYDWFERQLG	No linker
RP28	2214	6-1	2-1	RLEEEWAWVQCEVYGRGCPSSGGSGSLDESFYDWFERQLG	EEE Stretch in D8
RP29	2215	6-1	2-1	SLDREWACVKCEVYGRGCPGCGSGSGSLDESFYDWFERQLG	Repeat isolate
RP30	2216	6-1	2-1	SLEEEWAQVECEVYGRGCPSSGGSGSLDESFYDWFERQLG	D8 by Design
RP31	2217	6-1	2-1	SLEEEWAQVECEVYGRGCPSSGGSGSLDESFYHWFDRQLR	D8 & RP9 by design
RP32	2218	6-1	2-1	SIEEEWAQIKCDVWGRGCPGSGSGSLDESFYHWFDRQLR	D8 & RP9 by design
RP33	2219	6-1	2-1	QLDLEWAWVQCEVYGRGCGSGSLDESFYDWFERQLG	3 amino acid linker
RP34	2220	6-1	2-1	QLDEEWAGVQCEVYGRGCSLSDESFYDWFERQLG	No linker
RP35	2221	6-1	2-1	RLEEEWRWVQCEVYGRGCAAGSGSGSLDESFYDWFERQLG	EEE Stretch in D8
RP36	2222	6-10	2-1	SLDQEWAWVQCEVYGRGCPSSGGSGSDSDWAGYEWFEQLD	D8 (W1->S)- Group 6 by design

Pep. = peptide; Form. = formula; Linker sequences are shown in bold and underlined; All dimers are linked C-N

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C. Determination of Amino Acid Preferences

For both monomer and dimer peptides, amino acid preferences for each peptide were determined as follows. The expected frequency of each of the 20 amino acids at that position was calculated based on codon usage and % doping for that library. This was then compared to the actual frequency of occurrence of each amino acid at every position after four rounds of biopanning. Any amino acid that occurred at a frequency >2-fold was considered preferred. Most preferred amino acid(s) were those that have the greatest fold enrichment after panning. Preferred amino acid sequences for RP9, D8, and Formula 10 (Group 6) peptides are shown below.

TABLE 17

Peptide	Sequence	SEQ ID NO:
RP9	GSLDESFYDWFERQLG	1559
Regular	GLA <u>DEDFY</u> E WFERQLR L	2223
w/ Peptide	G <u>QLDEDFY</u> E WFDRQL S A	2224
w/ Insulin	G <u>F</u> M DESFYEWFERQLR W A	2225

Table 17 shows preferred amino acid sequences for RP9 peptides. Residues in bold indicate strong preference; underlined residues indicate positions where more than one amino acid preference is seen. The first column indicates the conditions used for the panning procedure. "RP9" indicates sequence of the parent RP9; "Regular" indicates regular pan as described in methods for panning of random libraries; "w/ peptide" indicates panning in the presence of 2 nM RP9 peptide; "w/ insulin" indicates panning in the presence of 2 nM insulin.

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TABLE 18

Peptide	Sequence	SEQ ID NO:
D8 Parent:	WLDQEWAWVQCEVYGRGCPS	2129
Dimer Consensus	sLEEE W aQIE CEVY /WGRGCps	2226
Monomer Consensus	sLEEE W aQIq CEIY /WGRGCry W	1548

Table 18 shows preferred amino acid sequences for D8 peptides. Upper case residues in bold indicate strong preference (>90% frequency); upper case letters, non-bold, indicate some preference (5-15% higher frequency than expected); lower case letters indicate less preference (2-5% higher frequency than expected); similar preferences seen in D8 in both monomer and dimer libraries. The underlined Y/W indicates that both residues are equally preferred at that position. In the original D8 sequence that position is occupied by Y.

TABLE 19

Peptide	Sequence	Type	SEQ ID NO:
Group 6	W(A/E)GYEW(F/L)	preferred core	1549
Group 6	DSDWAGYEWFEELD	preferred sequence	1595

Table 19 shows preferred amino acid sequences for Group 6 peptides. Underlined residues indicate preferred N-terminal and C-terminal extensions.

Example 12: Fluorescence-Based HIGF-1R Binding Assays

A. Heterogeneous Time-Resolved Fluorometric Assays

The effect of recombinant peptide surrogate G33 (rG33) on the binding of biotinylated-recombinant human IGF-1 (b-rhIGF-1) to recombinant

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human IGF-1R (rhIGF-1R) was determined using heterogeneous time-resolved fluorometric assays (TRF; DELFIA®, PE Wallac, Inc.). The rhIGF-1R protein included the extracellular domain of the receptor pre-propeptide, up to amino acid residue 932 (A. Ullrich *et al.*, 1986, *EMBO J.* 5:2503-2512).

- 5 Duplicate data points were collected at each concentration of competitor and the lines were designed to represent the best fit to a four-parameter non-linear regression analysis ($y = \min + (\max - \min) / (1 + 10^{((\log IC_{50} - x) * \text{Hillslope}))})$) of the data, which was used to determine IC_{50} values.

The assay was performed using a 96-well clear microplate (NUNC
10 MaxiSorp) with a final volume of 100 μ l. Microtiter plates were coated with 0.1 μ g rhIGF-1R in 100 μ l of $NaHCO_3$, pH 8.5 buffer, and incubated overnight at room temperature (RT). The plates were washed 3-times with 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl (TBS). This was followed by addition of 200 μ l blocking buffer (TBS containing 0.05%
15 Bovine Serum Albumin (BSA, Cohn Fraction V)), and incubated for 1 hr at RT. The plates were washed 6-times with a 1 X solution of Wallac's DELFIA® wash concentrate. Competitor was added in a volume of 50 μ l and serially diluted across the microtiter plate in TBS containing 0.05% BSA. Non-specific binding (background) was determined in the presence of 60 μ M
20 hIGF-1.

Fifty microliters of b-rhIGF-1, 10 nM, diluted in TBS containing 0.05% BSA was added. The plates were incubated for 2 hr at RT. After incubation, plates were washed 6-times with a 1X solution of Wallac's DELFIA® wash concentrate. Then the plates were treated with 100 μ L of
25 Wallac's DELFIA® Assay Buffer containing a 1:1000 dilution of europium-labeled streptavidin and incubated for 2 hours at RT. This was followed by washing 6-times with a 1 X solution of Wallac's DELFIA® wash concentrate. One hundred microliters of Wallac's DELFIA® enhancer was added, and the plates were shaken for 30 min at RT. After shaking, the fluorescence signal
30 at 620 nm was read on a Victor² 1420 plate reader (PE Wallac, Inc.).

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Primary data were background corrected, normalized to buffer controls, and then expressed as % Specific Binding. The Z'-factor was greater than 0.5 ($Z' = 1 - (3\sigma_+ + 3\sigma_-) / |\mu_+ - \mu_-|$; Zhang *et al.*, 1999, *J. Biomol. Screen.* 4:67-73) and the signal-to-background (S/B) ratio was ~20. The results of these experiments are shown in Figure 45. The IC₅₀ value calculated for rG33 is shown in Table 20, below.

The effect of recombinant peptide surrogates D815 (rD815), RP9, D815-6aa-G33, D815-6aa-RP9, and D815-12aa-RP9 on the binding of b-rhIGF-1 to rhIGF-1R was determined using the fluorometric assay described above. IGF-1 was used as a control. Duplicate data points were collected at each concentration of competitor and the lines represent the best fit to a four-parameter non-linear regression analysis, which was used to determine IC₅₀ values. Results for rD815 are shown in Figure 46; results for RP9 are shown in Figure 47; results for D815-6-G33 are shown in Figure 48; results for D815-6-RP9 are shown in Figure 49; and results for D815-12-RP9 are shown in Figure 50; the results for IGF-1 are shown in Figure 51. The IC₅₀ values for the rD815, RP9, D815-6aa-G33, D815-6aa-RP9, and D815-12aa-RP9 peptides, and IGF-1 are shown in Table 20, below. Linker sequences are underlined.

20

TABLE 20

Competitor	Sequence	SEQ ID NO:	IC ₅₀ (M)
rG33	GIISQSCPESFYDWFAGQVSDPWWCW	1600	1.45×10^{-6} M
rD815	WLDQERAWLWCEISGRGCLS	2206	4.08×10^{-6} M
RP9	GSLDESFYDWFERQLG	1559	4.17×10^{-7} M
D815-6aa-G33	WLDQERAWLWCEISGRGCLSGGSGGSGIIS QSCPESFYDWFAGQVSDPWWCW	2210	6.24×10^{-7} M
D815-6aa-RP9	WLDQERAWLWCEISGRGCLSGGSGGSGSL DESFYDWFERQLGKK	2211	3.57×10^{-8} M
D815-12aa-RP9	WLDQERAWLWCEISGRGCLSGGSGGSGG SGGSGSLDESFYDWFERQLGKK	2212	3.22×10^{-9} M
IGF-1			6.85×10^{-10} M

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The order of potency of all peptides or dimers compared to IGF-1 was determined as: IGF-1 > D815-12aa-RP9 >> D815-6aa-RP9 > RP9 \cong D815-6aa-G33 > rG33 > rD815. These results suggest that the coupling of D815 with RP9 using an extended linker (12 versus 6 amino acids) produced a
5 potent competitor that approximates the affinity of IGF-1 for its own receptor.

B. Time-Resolved Fluorescence Resonance Energy Transfer Assays

The effect of Site 1 peptide surrogates, Site 2 peptide surrogates, and
10 rhIGF-1 on the dissociation of biotinylated-20E2 (b-20E2, Site 1) from recombinant human IGF-1R was determined using time-resolved fluorescence resonance energy transfer assays (TR-FRET). Best fit non-linear regression analysis of the data, was used to determine dissociation rate constants. Each data point represents a single observation.

15 The assay was performed using a 96-well white microplate (NUNC) with a final volume of 100 μ l. Final incubation conditions were 16.5 nM b-20E2, 2.2 nM SA-APC (streptavidin-allophycocyanin), 2.2 nM Eu³⁺-rhIGF-1R (LANCETTM labeled, PE Wallac, Inc.), 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, and 0.1 % BSA (Cohn Fraction V). Reactions were
20 allowed to reach equilibrium for 6 hr at RT. Following this, various peptide surrogates or IGF-1 were added at a final concentration of 100 μ M or 30 μ M, respectively. The addition of peptides or IGF-1 initiated the measurement of dissociation (Time Zero, sec). The fluorescence signal at 665 nm was read on a Victor² 1420 plate reader (PE Wallac, Inc.) at 30 sec intervals.

25 Results of these experiments are shown in Figure 52. The buffer controls did not vary over the time interval of study, which demonstrated that the equilibrium was not disturbed by the addition of diluent at Time zero. The addition of excess (> 1000-fold 20E2 K_d for IGF-1R) Site 1 peptides such as H2C, 20E2, or RP6 did not differ depending on specific the peptide
30 used, and the dissociation rates of b-20E2 were similar for these peptides. D8B12 (Site 2 peptide) and IGF-1 (binds both Site 1 and Site 2) did

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demonstrate significant differences in the rate of dissociation of b-20E2. This would suggest that these agents act as non-competitive or allosteric regulators of Site 1 binding.

The effect of various peptide surrogates or peptide dimers on the binding of biotinylated-20E2 (B-20E2) to recombinant human IGF-1R was determined using TR-FRET assays, described above. For these experiments, each data point represents the average of two replicate wells. The lines represent the best fit to a four-parameter non-linear regression analysis ($y = \min + (\max - \min) / (1 + 10^{((\log IC_{50} - x) * \text{Hillslope}))})$) of the data, which was used to determine IC_{50} values.

The assays were performed using a 384-well white microplate (NUNC) with a final volume of 30 μ l. Final incubation conditions were 15 nM b-20E2, 2 nM SA-APC, 2 nM Eu^{3+} -rhIGF-1R (LANCE™ labeled, PE Wallac, Inc.), 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, and 0.1 % BSA (Cohn Fraction V). After 16-24 hr of incubation at RT, the fluorescence signal at 665 nm and 620 nm was read on a Victor² 1420 plate reader (PE Wallac, Inc.). Primary data were background corrected, normalized to buffer controls, and then expressed as % Specific Binding. The Z'-factor was greater than 0.5 ($Z' = 1 - (3\sigma_+ + 3\sigma_-) / |\mu_+ - \mu_-|$; Zhang et al, 1999, *J. Biomol. Screen.* 4:67-73) and the signal-to-background (S/B) ratio was ~ 4. Results of these experiments are shown in Figure 53. Table 21, below, shows the IC_{50} values calculated for these experiments. Notably, the C1 peptide showed IGF-1R affinities of ~1 nM (Figure 53) and ~10 nM (Table 21) in these assays.

25

TABLE 21

Competitor	Sequence	SEQ ID NO:	Formula	Site IGF-1R	IC_{50} (M)
C1	CWARPCGDAANFYDWFVQQAS	1550	1	1	8.80E-10
IGF-1					2.93E-09
RP9	GSLDESFYDWFERQLG	1559	1	1	3.93E-08

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20E2	DYKDFYDAIDQLVRGSARAGGTRD	2209	2	1	1.04E-07
E8	GGTVWPGYEWLRNA	2118	10	2	2.53E-07
H2C	FHENFYDWFVQRVSKK	2117	1	1	4.60E-07
S173	LDALDRLMRYFEERPSL	1830	3	1	6.29E-06
D8B12	WLEQERAWIWCEIQGSGCRA	1884	6	2	1.13E-05
A6	SAKNFYDWFVKK	1551	1	1	3.10E-05

C. Fluorescence Polarization Assays

The effect of various peptide monomers and dimers on the binding of fluorescein-RP-9 (FITC-RP9) to soluble human insulin receptor-immunoglobulin heavy chain chimera (sIR-Fc; Bass *et al.*, 1996, *J. Biol. Chem.* **271**:19367-19375) was determined using fluorescence polarization assays (FP). For these experiments, each data point represents the average of two replicate wells. The lines represent the best fit to a four-parameter non-linear regression analysis of the data, which was used to determine IC₅₀ values.

The assays were performed in a 384-well black microplate (NUNC) with a final volume of 30 μ l. Final incubation conditions were 1 nM FITC-RP9, 10 nM sIR, 0.05 M Tris-HCl (pH 8 at 25°C), 0.138 M NaCl, 0.0027 M KCl, 0.05 % BGG (bovine gamma globulin), 0.005 % Tween-20[®]. After 16-24 hr of incubation at RT, the fluorescence signal at 520 nm was read on an Analyst[™] AD plate reader (LJL BioSystems, Inc.). Primary data were background corrected using 10 nM sIR without FITC-RP9 addition, normalized to buffer controls and then expressed as % Specific Binding. The Z'-factor was greater than 0.5 ($Z' = 1 - (3\sigma_+ + 3\sigma_-) / |\mu_+ - \mu_-|$; Zhang *et al.*, 1999, *J. Biomol. Screen.* **4**:67-73) and the assay dynamic range was ~125 mP. In parallel with these experiments, TR-FRET assays were performed using rhIGF-1R and b-20E2, as described above. Results of the FP and TR-FRET experiments are shown in Table 22, below.

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TABLE 22

Peptide	FP sIR-Fc	TR-FRET rhIGF-1R	Binding Ratio IGF-1R / IR	Formula	Site IGF-1R	SEQ ID NO:	Sequence
RP4	17	8100	476	2	1	1552	PPWGARFYDAIEQLVFDNL
S175	10	1650	165	1	1	1560	GRVDWLQRNANFYDWFVA ELG
RP15	28	706	25	1	1	2130	SQAGSAFYAWFDQVLRTV
H2C (D117)	66	600	9	1	1	2117	FHENFYDWFVQRVSKK
20E2 (D118)	51	100	1.9	2	1	2209	DYKDFYDAIDQLVRGSARA GGTRD
RP9	24	33	1.4	1	1	1559	GSLDESFYDWFERQLG
G33	139	178	1.3	1	1	1600	GIISQSCPESFYDWFAGQV SDPWWCW
E8 (D120)	206	175	0.85	10	2	2118	GGTVWPGYEWLRNA
C1 (D112)	52	10	0.19	1	1	1550	CWARPCGDAANFYDWFV QQAS
RP16	6400	961	0.15			1553	VMDARDDPFYHKLSELVT

5 FP sIR-Fc column shows IC₅₀ (nM) values obtained (vs. FITC-RP9); TR-FRET rhIGF-1R column shows IC₅₀ (nM) values obtained (vs. b-20E2); for Binding Ratio: higher values indicated higher affinity for IR than IGF-1R.

10 These results demonstrated that S175, RP4, and RP15 showed high affinities for IR and showed high binding ratios for IGF-1R over IR. H2C, 20E2, RP9, and C1 were slightly less potent than S175, RP4, and RP15 at IR, and these peptides had lower binding ratios for IGF-1R over IR. G33 and E8 were less potent than S175, RP4, and RP15 at IR, and showed comparable binding to IGF-1R and IR. RP16 had poor potency at IR and IGF-1R, but had higher affinity for IGF-1R than IR.

Example 13: Insulin Receptor Surrogates with Enhanced Specificity

15 Peptide S597 was tested for its bioactivity relative to insulin. SGBS cells (a human adipocyte cell line) were incubated with various concentrations of human insulin or peptide S597 and cellular uptake of ¹⁴C-glucose was measured essentially as described in Example 4. The results

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(as illustrated in Figure 54) indicate that the potency of S597 in stimulating glucose uptake is at least as good as that of human insulin.

The glucose-lowering effect of peptide S597 and peptide S557 in rats was compared with that of insulin as follows: Eighteen male Wistar rats, 200-225 g, fasted for 18 h, were anesthetized using Hypnorm-Dormicum (1.25 mg/ml Dormicum, 2.5 mg/ml fluanisone, 0.079 mg/ml fentanyl citrate) 2 ml/kg as a priming dose 30 min prior to test substance dosing and additional 1 ml/kg every 20 minutes (at time points -10 min, 10 min and 30 min relative to test substance dosing).

The rats were allocated into three groups. The animals were dosed with an intravenous injection (tail vein), 2 ml/kg, of either human insulin 1.25 nmol/kg (n=6) or S557 peptide 5 nmol/kg (n=6) or S597 peptide 5 nmol/kg (n=6). Blood samples for the determination of whole blood glucose concentration were collected in heparinized 10 µl glass tubes by puncture of the capillary vessels in the tail tip at times -20 min and 0 min (before dosing), and at times 10, 20, 30, 40, 60, 80, 120, and 180 min after dosing. Blood glucose concentrations were measured after dilution in analysis buffer by the immobilized glucose oxidase method using an EBIO Plus autoanalyzer (Eppendorf, Germany).

The results (as illustrated in Figure 55) indicate that the blood glucose lowering effect of S597 in rats is about 4 times lower than that of human insulin. The improved effect of S597 relative to S557 shows the effect of N-terminal acetylation.

The glucose-lowering effect of different concentrations of peptide S597 was also tested by intravenous administration to fasted Goettingen minipigs weighing about 15 kg. The results (as illustrated in Figure 56) indicate that the glucose-lowering effect at 3 nmol/kg S597 is comparable to that of 0.3 nmol/kg human insulin.

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Example 14: Co-administration of Therapeutic Peptides

The rate of disappearance of two co-administered peptides was tested as follows:

Mixtures containing 600 nmol/ml peptide S557 and 1800 nmol/ml B²⁹-
5 N -(N-lithocolyl- -glutamyl)-des(B30) human insulin included ¹²⁵I-labeled
peptides were injected into the neck of a pig. Radioactivity at the injection
site was monitored over time using an external gamma counter.

The results (as illustrated in Figure 57) indicate that the
disappearance of either peptide was not influenced by the presence of the
10 second peptide.

Incorporated herein by reference in its entirety is the Sequence
Listing for the application, comprising SEQ ID NO:1 to SEQ ID NO:2227.
The Sequence Listing is disclosed on three CD-ROMs, designated "CRF",
15 "Copy 1", and "Copy 2". The Sequence Listing is a computer-readable
ASCII file named "18784057PC.app.txt", created on September 23, 2002, in
IBM-PC machine format, on a MS-Windows®98 operating system. The
18784057PC.app.txt file is 927,476 bytes in size.

20 As various changes can be made in the above compositions and
methods without departing from the scope and spirit of the invention, it is
intended that all subject matter contained in the above description, shown in
the accompanying drawings, or defined in the appended claims be
interpreted as illustrative, and not in a limiting sense.

25

The contents of all patents, patent applications, published articles,
books, reference manuals, texts and abstracts cited herein are hereby
incorporated by reference in their entirety to more fully describe the state of
the art to which the present invention pertains.

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WHAT IS CLAIMED IS:

1. A method of decreasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence in an amount sufficient to decrease insulin activity, wherein the amino acid sequence comprises a subsequence that comprises a sequence that binds to Site 1 of insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin receptor, and wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 1 to Site 2, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.
2. The method according to claim 1, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
3. The method according to claim 2, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.

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4. The method according to claim 2, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
5. The method according to claim 2, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
6. The method according to claim 2, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAWVQCEVYGRGCPS (SEQ ID NO:2129).
7. The method according to claim 2, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
8. The method according to claim 2, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NOS:926-1061 (Figures 3A-3E); SEQ ID NOS:1244-1253 (Figure 9A); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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9. The method according to claim 2, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).
10. The method according to claim 2, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NOS:1909-1910), S515 (SEQ ID NO:2102), and RB426 (SEQ ID NO:2158).

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11. The method according to claim 2, wherein the Formula 1 sequence is selected from the group consisting of sequences

H2C/D117:

FHENFYDWFVRQVSKK (SEQ ID NO:1556);
 FHENFYDWFVRQVS (SEQ ID NO:1557);
 RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
 GSLDESFYDWFERQLG (SEQ ID NO:1559);
 GLADED FYEWFERQLR (SEQ ID NO:1561);
 GLADELFYEWFD RQLS (SEQ ID NO:1562);
 GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
 GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
 GFMDSEFYEWFERQLR (SEQ ID NO:1565);
 GFWDESFYAWFERQLR (SEQ ID NO:1566);
 GFMDSEFYAWFERQLR (SEQ ID NO:1567);
 GFWDESFYEWFERQLR (SEQ ID NO:1568);
 RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2130); and
 S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

12. The method according to claim 2, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:

WLDQEWVQCEVYGRGCPSKK (SEQ ID NO:2227);
 KWLDQEAWVQCEVYGRGCPSKK (SEQ ID NO:1579);
 KWLDQEAWVQCEVYGRGCPS (SEQ ID NO:1580);
 SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
 SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
 SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
 SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584).

13. The method according to claim 2, wherein the amino acid sequence is selected from the group consisting of sequences 537-538 (SEQ ID NOS:2114-2115).

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14. The method according to claim 2, wherein the amino acid sequence is selected from the group consisting of sequences S425 (SEQ ID NO:2031), S454 (SEQ ID NOS:2058-2059), S459 (SEQ ID NO:2065), and RB537-RB538 (SEQ ID NOS:2197-2198).
15. The method according to claim 1, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are any amino acid; X_{23} is any hydrophobic amino acid; X_{27} is a polar amino acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid; and wherein at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or X_{40} .
16. The method according to claim 15, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
17. The method according to claim 15, wherein X_{24} and X_{39} are cysteines, X_{23} is selected from leucine, isoleucine, methionine and valine; X_{27} is selected from glutamic acid, aspartic acid, asparagine, and glutamine; X_{31} is tryptophan, X_{32} is glycine; and X_{36} is any aromatic amino acid.
18. The method according to claim 15, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
19. The method according to claim 15, wherein the Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$ is HLCVLEELFWGASLFGYCSG (SEQ ID NO:1576).

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20. The method according to claim 15, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
21. The method according to claim 15, wherein the Formula 4 sequence is selected from the group consisting of sequences SEQ ID NOS:713-925 (Figures 2A-2E); SEQ ID NOS:1254-1261 (Figure 9B); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
22. The method according to claim 15, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO: 1600), S342 (SEQ ID NO: 1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170AA), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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23. The method according to claim 15, wherein the Formula 4 sequence is selected from the group consisting of sequences S262 (SEQ ID NO:1898), S282-S283 (SEQ ID NOS:1907-1908), S331 (SEQ ID NO:1949), RB505M (SEQ ID NO:2160), RB446 (SEQ ID NO:2180), and RB505 (SEQ ID NO:2191).
24. The method according to claim 15, wherein the Formula 4 sequence is selected from the group consisting of sequences RB517M (SEQ ID NO:2161), RB515 (SEQ ID NO:2162), and RB510 (SEQ ID NO:2163).
25. The method according to claim 15, wherein the Formula 1 sequence is selected from the group consisting of sequences
H2C/D117:
FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADEDFYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFDQRQLS (SEQ ID NO:1562);
GQLDEDFYEWFDQRQLS (SEQ ID NO:1563);
GQLDEDFYAWFDQRQLS (SEQ ID NO:1564);
GFMDESFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDESFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2130); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).
26. The method according to claim 15, wherein the amino acid sequence is selected from the group consisting of sequences 431-433 (SEQ ID NOS:2135-2137).

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27. The method according to claim 15, wherein the amino acid sequence is selected from the group consisting of sequences RB431-RB433 (SEQ ID NOS:2184, 2186 and 2188).
28. A method of increasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence in an amount sufficient to increase insulin activity, wherein the amino acid sequence comprises a subsequence that comprises a sequence that binds to Site 1 of insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin receptor, and wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 2 to Site 1, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.
29. The method according to claim 28, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
30. The method according to claim 29, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.

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31. The method according to claim 29, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
32. The method according to claim 29, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
33. The method according to claim 29, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAWVQCEVYGRGCPS (SEQ ID NO:2129).
34. The method according to claim 29, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
35. The method according to claim 29, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NOS:926-1061 (Figures 3A-3E); SEQ ID NOS:1244-1253 (Figure 9A); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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36. The method according to claim 29, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1990-1991), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, 1900-1901), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).
37. The method according to claim 29, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NOS:1909-1910), S515 (SEQ ID NO:2102), and RB426 (SEQ ID NO:2158).

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38. The method according to claim 29, wherein the Formula 1 sequence is selected from the group consisting of sequences

H2C/D117:

FHENFYDWFVRQVSKK (SEQ ID NO:1556);
 FHENFYDWFVRQVS (SEQ ID NO:1557);
 RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
 GSLDESFYDWFERQLG (SEQ ID NO:1559);
 GLADEDFYEWFERQLR (SEQ ID NO:1561);
 GLADELFYEWFDRLS (SEQ ID NO:1562);
 GQLDEDFYEWFDRLS (SEQ ID NO:1563);
 GQLDEDFYAWFDRLS (SEQ ID NO:1564);
 GFMDSEFYEWFERQLR (SEQ ID NO:1565);
 GFWDESFYAWFERQLR (SEQ ID NO:1566);
 GFMDSEFYAWFERQLR (SEQ ID NO:1567);
 GFWDESFYEWFERQLR (SEQ ID NO:1568);
 RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2130); and
 S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

39. The method according to claim 29, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:

WLDQEWVQCEVYGRGCPSKK (SEQ ID NO:2227);
 KWLDQEWAWVQCEVYGRGCPSKK (SEQ ID NO:1579);
 KWLDQEWAWVQCEVYGRGCPS (SEQ ID NO:1580);
 SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
 SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
 SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
 SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584).

40. The method according to claim 29, wherein the amino acid sequence is sequence 539 (SEQ ID NO:2116).

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41. The method according to claim 29, wherein the amino acid sequence is selected from the group consisting of sequences RP27 (SEQ ID NO:2213), RP28 (SEQ ID NO:2214), RP29 (SEQ ID NO:2215), RP30 (SEQ ID NO:2216), RP31 (SEQ ID NO:2217), RP32 (SEQ ID NO:2218), RP33 (SEQ ID NO:2219), RP34 (SEQ ID NO:2220), RP35 (SEQ ID NO:2221), and RP36 (SEQ ID NO:2222).
42. The method according to claim 29, wherein the amino acid sequence is selected from the group consisting of sequences D8-6aa-S175 (SEQ ID NO:2121), D8-12aa-S175 (SEQ ID NO:2122), D8-6aa-RP6 (SEQ ID NO:2126), and D8-6aa-RP17 (SEQ ID NO:2127).
43. The method according to claim 29, wherein the amino acid sequence is selected from the group consisting of sequences S429 (SEQ ID NO:2032), S455 (SEQ ID NO:2060), S457-S458 (SEQ ID NOS:2063-2064), S467-S468 (SEQ ID NOS:2066-2067), S471 (SEQ ID NO:2068), S481-S513 (SEQ ID NOS:2069-2101), S517-S520 (SEQ ID NOS:2104-2107), S524 (SEQ ID NO:2111), RB539 (SEQ ID NO:2196), RB625-RB626 (SEQ ID NOS:2200 and 2199), and RB622 (SEQ ID NO:2201).
44. The method according to claim 28, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are any amino acid; X_{23} is any hydrophobic amino acid; X_{27} is a polar amino acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid; and wherein at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or X_{40} .

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45. The method according to claim 44, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
46. The method according to claim 45, wherein X_{24} and X_{39} are cysteines, X_{23} is selected from leucine, isoleucine, methionine and valine; X_{27} is selected from glutamic acid, aspartic acid, asparagine, and glutamine; X_{31} is tryptophan, X_{32} is glycine; and X_{36} is any aromatic amino acid.
47. The method according to claim 45, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
48. The method according to claim 45, wherein the Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33} X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$ is HLCVLEELFWGASLFGYCSG (SEQ ID NO:1576).
49. The method according to claim 45, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
50. The method according to claim 45, wherein the Formula 4 sequence is selected from the group consisting of sequences SEQ ID NOS:713-925 (Figures 2A-2E); SEQ ID NOS:1254-1261 (Figure 9B); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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51. The method according to claim 45, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:204).
52. The method according to claim 45, wherein the Formula 4 sequence is selected from the group consisting of sequences S262 (SEQ ID NO:1898), S282-S283 (SEQ ID NOS:1907-1908), S331 (SEQ ID NO:1949), RB505M (SEQ ID NO:2160), RB446 (SEQ ID NO:2180), and RB505 (SEQ ID NO:2191).
53. The method according to claim 45, wherein the Formula 4 sequence is selected from the group consisting of sequences RB517M (SEQ ID NO:2161), RB515 (SEQ ID NO:2162), and RB510 (SEQ ID NO:2163).

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54. The method according to claim 45, wherein the Formula 1 sequence is selected from the group consisting of sequences
- H2C/D117: FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADED FYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFD RQLS (SEQ ID NO:1562);
GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
GFMDESFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDESFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2130); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).
55. The method according to claim 45, wherein the amino acid sequence is selected from the group consisting of sequences F8-6aa-RP9 (SEQ ID NO:2119), F8-12aa-RP9 (SEQ ID NO:2120), F8-6aa-S175 (SEQ ID NO:2123), F8-12aa-S175 (SEQ ID NO:2124), S516 (SEQ ID NO:2103), S521 (SEQ ID NO:2108), and S522 (SEQ ID NO:2109).
56. A method of increasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence in an amount sufficient to increase insulin activity, wherein the amino acid sequence comprises a plurality of subsequences that each comprise a sequence that binds to Site 1 of insulin receptor, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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57. The method according to claim 56, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid.
58. The method according to claim 57, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
59. The method according to claim 57, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
60. The method according to claim 57, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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61. The method according to claim 57, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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62. The method according to claim 57, wherein the Formula 1 sequence is selected from the group consisting of sequences

H2C/D117:

FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADED FYEWFERQLR (SEQ ID NO:1561);
GLADEL FYEWFDRQLS (SEQ ID NO:1562);
GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
GFMDESFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDESFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2130); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

63. The method according to claim 57, wherein the amino acid sequence is selected from the group consisting of sequences 521 (SEQ ID NO:2112) and 535 (SEQ ID NO:2113).

64. The method according to claim 57, wherein the amino acid sequence is selected from the group consisting of sequences 434 (SEQ ID NO:2138), 436 (SEQ ID NO:2139), 427 (SEQ ID NO:2141), 435 (SEQ ID NO:2142), 439 (SEQ ID NO:2143), 449 (SEQ ID NO:2144), and 463 (SEQ ID NO:2146).

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65. The method according to claim 57, wherein the amino acid sequence is selected from the group consisting of sequences S128 (SEQ ID NOS:1817-1818), S145 (SEQ ID NOS:1822-1823), S169-S170 (SEQ ID NOS:1827-1830), S172 (SEQ ID NOS:1832-1833), S218 (SEQ ID NOS:1850-1851), S228 (SEQ ID NOS:1859-1860), S231-232 (SEQ ID NOS:1863-1866), S253 (SEQ ID NOS:1889-1890), S267 (SEQ ID NO:), S290-S293 (SEQ ID NOS:1914-1921), S300-S301 (SEQ ID NOS:1924-1927), S312 (SEQ ID NOS:1933-1934), S325 (SEQ ID NOS:1944-1945), S329 (SEQ ID NOS:1947-1948), S332-S337 (SEQ ID NOS:1950-1961), S349-S354 (SEQ ID NOS:1965-1976), S359-S363 (SEQ ID NOS:1977-1986), S374-S376 (SEQ ID NOS:1992-1996), S378-S381 (SEQ ID NOS:1997-2004), S414-S418 (SEQ ID NOS:2015-2024), S420 (SEQ ID NOS:2027-2028), RB463 (SEQ ID NO:2165), RB439 (SEQ ID NO:2166), RB436 (SEQ ID NO:2167), RB449 (SEQ ID NO:2168), RB508M-RB509M (SEQ ID NOS:2171-2172), RB508-RB509 (SEQ ID NOS:2189-2190), RB521 (SEQ ID NO:2193), and RB535 (SEQ ID NO:2194).
66. A method of increasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence in an amount sufficient to increase insulin activity, wherein the amino acid sequence comprises a subsequence that comprises a sequence that binds to Site 1 of insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin receptor, wherein the subsequences are linked C-terminus to C-terminus or N-terminus to N-terminus, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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67. The method according to claim 66, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
68. The method according to claim 67, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
69. The method according to claim 67, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
70. The method according to claim 67, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
71. The method according to claim 67, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAWVQCEVYGRGCPs (SEQ ID NO:2056).
72. The method according to claim 67, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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73. The method according to claim 67, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NOS:926-1061 (Figures 3A-3E); SEQ ID NOS:1244-1253 (Figure 9A); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
74. The method according to claim 67, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO: 1600), S342 (SEQ ID NO: 1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).
75. The method according to claim 67, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NOS:1909-1910), S515 (SEQ ID NO:2102) and RB426 (SEQ ID NO:2158).

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76. The method according to claim 67, wherein the Formula 1 sequence is selected from the group consisting of sequences

H2C/D117:

FHENFYDWFVRQVSKK (SEQ ID NO:1556);
 FHENFYDWFVRQVS (SEQ ID NO:1557);
 RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
 GSLDESFYDWFERQLG (SEQ ID NO:1559);
 GLADED FYEWFERQLR (SEQ ID NO:1561);
 GLADELFYEWFD RQLS (SEQ ID NO:1562);
 GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
 GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
 GFMDESFYEWFERQLR (SEQ ID NO:1565);
 GFWDESFYAWFERQLR (SEQ ID NO:1566);
 GFMDESFYAWFERQLR (SEQ ID NO:1567);
 GFWDESFYEWFERQLR (SEQ ID NO:1568);
 RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
 S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

77. The method according to claim 67, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:

WLDQEWWQCEVYGRGCPSKK (SEQ ID NO:2227);
 KWLDQEWA WQCEVYGRGCPSKK (SEQ ID NO:1579);
 KWLDQEWA WQCEVYGRGCPS (SEQ ID NO:1580);
 SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
 SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
 SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
 SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584).

78. The method according to claim 67, wherein the amino acid sequence is selected from the group consisting of sequences S432-S433 (SEQ ID NOS:2033-2036), S436-S445 (SEQ ID NOS:2037-2056), and S456 (SEQ ID NOS:2061-2062).

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79. An amino acid sequence that is an insulin receptor agonist, which comprises a subsequence that comprises a sequence that binds to Site 1 of the insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of the insulin receptor, wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 2 to Site 1, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.
80. The amino acid sequence according to claim 79, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
81. The amino acid sequence according to claim 80, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
82. The amino acid sequence according to claim 80, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
83. The amino acid sequence according to claim 80, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).

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84. The amino acid sequence according to claim 80, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAWVQCEVYGRGCPS (SEQ ID NO:2056).
85. The amino acid sequence according to claim 80, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
86. The amino acid sequence according to claim 80, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NOS:926-1061 (Figures 3A-3E); SEQ ID NOS:1244-1253 (Figure 9A); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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87. The amino acid sequence according to claim 80, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).
88. The amino acid sequence according to claim 80, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NOS:1909-1910), S515 (SEQ ID NO:2102), and RB426 (SEQ ID NO:2158).

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89. The amino acid sequence according to claim 80, wherein the Formula 1 sequence is selected from the group consisting of sequences H2C/D117:
 FHENFYDWFVRQVSKK (SEQ ID NO:1556);
 FHENFYDWFVRQVS (SEQ ID NO:1557);
 RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
 GSLDESFYDWFERQLG (SEQ ID NO:1559);
 GLADEDFYEWFERQLR (SEQ ID NO:1561);
 GLADELFYEWFDQRQLS (SEQ ID NO:1562);
 GQLDEDFYEWFDQRQLS (SEQ ID NO:1563);
 GQLDEDFYAWFDQRQLS (SEQ ID NO:1564);
 GFMDSEFYEWFERQLR (SEQ ID NO:1565);
 GFWDESFYAWFERQLR (SEQ ID NO:1566);
 GFMDSEFYAWFERQLR (SEQ ID NO:1567);
 GFWDESFYEWFERQLR (SEQ ID NO:1568);
 RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
 S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).
90. The amino acid sequence according to claim 80, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:
 WLDQEWVQCEVYGRGCPSKK
 (SEQ ID NO:2227); KWLDQEWAWVQCEVYGRGCPSKK (SEQ ID NO:1579); KWLDQEWAWVQCEVYGRGCPS (SEQ ID NO:1580);
 SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
 SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
 SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
 SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584).
91. The amino acid sequence according to claim 80, wherein the amino acid sequence is sequence 539 (SEQ ID NO:2116).

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92. The amino acid sequence according to claim 80, wherein the amino acid sequence is selected from the group consisting of sequences S429 (SEQ ID NO:2032), S455 (SEQ ID NO:2060), S457-S458 (SEQ ID NOS:2063-2064), S467-S468 (SEQ ID NOS:2066-2067), S471 (SEQ ID NO:2068), S471 (SEQ ID NO:2068), S481-S513 (SEQ ID NOS:2069-2101), S517-S520 (SEQ ID NOS:2104-2107), S524 (SEQ ID NO:2111), RB539 (SEQ ID NO:2196), RB625-RB626 (SEQ ID NOS:2200 and 2199), and RB622 (SEQ ID NO:2201).
93. The amino acid sequence according to claim 80, wherein the amino acid sequence is selected from the group consisting of sequences RP27 (SEQ ID NO:2213), RP28 (SEQ ID NO:2214), RP29 (SEQ ID NO:2215), RP30 (SEQ ID NO:2216), RP31 (SEQ ID NO:2217), RP32 (SEQ ID NO:2218), RP33 (SEQ ID NO:2219), RP34 (SEQ ID NO:2220), and RP35 (SEQ ID NO:2221).
94. The amino acid sequence according to claim 80, wherein the amino acid sequence is selected from the group consisting of sequences D8-6aa-S175 (SEQ ID NO:2121), D8-12aa-S175 (SEQ ID NO:2122), D8-6aa-RP15 (SEQ ID NO:2126), and D8-6aa-RP17 (SEQ ID NO:2127).
95. The amino acid sequence according to claim 79, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are any amino acid; X_{23} is any hydrophobic amino acid; X_{27} is a polar amino acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid; and wherein at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or X_{40} .

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96. The amino acid sequence according to claim 95, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
97. The amino acid sequence according to claim 95, wherein X_{24} and X_{39} are cysteines, X_{23} is selected from leucine, isoleucine, methionine and valine; X_{27} is selected from glutamic acid, aspartic acid, asparagine, and glutamine; X_{31} is tryptophan, X_{32} is glycine; and X_{36} is any aromatic amino acid.
98. The amino acid sequence according to claim 95, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
99. The amino acid sequence according to claim 95, wherein the Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$ is HLCVLEELFWGASLFGYCSG (SEQ ID NO:1576).
100. The amino acid sequence according to claim 95, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
101. The amino acid sequence according to claim 95, wherein the Formula 4 sequence is selected from the group consisting of sequences S262 (SEQ ID NO:1898), S282-S283 (SEQ ID NOS:1907-1908), S331 (SEQ ID NO:1949), RB505M (SEQ ID NO:2160), RB446 (SEQ ID NO:2180), and RB505 (SEQ ID NO:2191).

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102. The amino acid sequence according to claim 95, wherein the Formula 4 sequence is selected from the group consisting of sequences RB517M (SEQ ID NO:2161), RB515 (SEQ ID NO:2162), and RB510 (SEQ ID NO:2163).
103. The amino acid sequence according to claim 95, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558 and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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104. The amino acid sequence according to claim 95, wherein the Formula 1 sequence is selected from the group consisting of sequences H2C/D117:
FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADED FYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFD RQLS (SEQ ID NO:1562);
GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
GFMDESFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDESFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).
105. The amino acid sequence according to claim 95, wherein the amino acid sequence is selected from the group consisting of sequences F8-6aa-RP9 (SEQ ID NO:2119), F8-12aa-RP9 (SEQ ID NO:2120), F8-6aa-S175 (SEQ ID NO:2123), F8-12aa-S175 (SEQ ID NO:2124), S516 (SEQ ID NO:2103), S521 (SEQ ID NO:2108), and S522 (SEQ ID NO:2109).
106. An amino acid sequence that is an insulin receptor agonist, which comprises a plurality of subsequences that each comprise a sequence that binds to Site 1 of insulin receptor, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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107. The amino acid sequence according to claim 106, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$, wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid.
108. The amino acid sequence according to claim 107, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
109. The amino acid sequence according to claim 107, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
110. The amino acid sequence according to claim 107, wherein the Formula 1 sequence is selected from the group consisting of SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NO:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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111. The amino acid sequence according to claim 107, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO: 1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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112. The amino acid sequence according to claim 107, wherein the Formula 1 sequence is selected from the group consisting of sequences

H2C/D117: FHENFYDWFVRQVSKK (SEQ ID NO:1556);

FHENFYDWFVRQVS (SEQ ID NO:1557);

RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);

GSLDESFYDWFERQLG (SEQ ID NO:1559);

GLADED FYEWFERQLR (SEQ ID NO:1561);

GLADEL FYEWFDRQLS (SEQ ID NO:1562);

GQLDEDFYEWFD RQLS (SEQ ID NO:1563);

GQLDEDFYAWFD RQLS (SEQ ID NO:1564);

GFMD ESYEWFERQLR (SEQ ID NO:1565);

GFWD ESYAWFERQLR (SEQ ID NO:1566);

GFMD ESYAWFERQLR (SEQ ID NO:1567);

GFWD ESYEWFERQLR (SEQ ID NO:1568);

RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and

S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

113. The amino acid sequence according to claim 107, wherein the amino acid sequence is selected from the group consisting of sequences 521 (SEQ ID NO:2112) and 535 (SEQ ID NO:2113).

114. The amino acid sequence according to claim 107, wherein the amino acid sequence is selected from the group consisting of sequences 434 (SEQ ID NO:2138), 436 (SEQ ID NO:2139), 427 (SEQ ID NO:2141), 435 (SEQ ID NO:2142), 439 (SEQ ID NO:2143), 449 (SEQ ID NO:2144), and 463 (SEQ ID NO:2146).

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115. The amino acid sequence according to claim 107, wherein the amino acid sequence is selected from the group consisting of sequences S128 (SEQ ID NOS:1817-1818), S145 (SEQ ID NOS:1822-1823), S169-S170 (SEQ ID NOS:1827-1830), S172 (SEQ ID NOS:1832-1833), S218 (SEQ ID NOS:1850-1851), S228 (SEQ ID NOS:1859-1860), S231-232 (SEQ ID NOS:1863-1866), S253 (SEQ ID NOS:1889-1890), S267 (SEQ ID NO:), S290-S293 (SEQ ID NOS:1914-1921), S300-S301 (SEQ ID NOS:1924-1927), S312 (SEQ ID NOS:1933-1934), S325 (SEQ ID NOS:1944-1945), S329 (SEQ ID NOS:1947-1948), S332-S337 (SEQ ID NOS:1950-1961), S349-S354 (SEQ ID NOS:1965-1976), S359-S363 (SEQ ID NOS:1977-1986), S374-S376 (SEQ ID NOS:1992-1996), S378-S381 (SEQ ID NOS:1997-2004), S414-S418 (SEQ ID NOS:2015-2024), S420 (SEQ ID NOS:2027-2028), RB463 (SEQ ID NO:2165), RB439 (SEQ ID NO:2166), RB436 (SEQ ID NO:2167), RB449 (SEQ ID NO:2168), RB508M-RB509M (SEQ ID NOS:2171-2172), RB508-RB509 (SEQ ID NOS:2189-2190), RB521 (SEQ ID NO:2193), and RB535 (SEQ ID NO:2194).
116. An amino acid sequence that is an insulin receptor agonist, which comprises a subsequence that comprises a sequence that binds to Site 1 of insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin receptor, wherein the subsequences are linked C-terminus to C-terminus or N-terminus to N-terminus, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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117. The amino acid sequence according to claim 116, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
118. The amino acid sequence according to claim 117, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
119. The amino acid sequence according to claim 117, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
120. The amino acid sequence according to claim 117, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
121. The amino acid sequence according to claim 117, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAVVQCEVYGRGCP (SEQ ID NO:2056).

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122. The amino acid sequence according to claim 117, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NO:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
123. The amino acid sequence according to claim 117, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NOS:926-1061 (Figures 3A-3E); SEQ ID NOS:1244-1253 (Figure 9A); and SEQ ID NO:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
124. The amino acid sequence according to claim 117, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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125. The amino acid sequence according to claim 117, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NO:DD-1909-1910), S515 (SEQ ID NO:2102), and RB426 (SEQ ID NO:2158).
126. The amino acid sequence according to claim 117, wherein the Formula 1 sequence is selected from the group consisting of sequences
- H2C/D117: FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADEDFYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFDRLS (SEQ ID NO:1562);
GQLDEDFYEWFDRLS (SEQ ID NO:1563);
GQLDEDFYAWFDRLS (SEQ ID NO:1564);
GFMDSEFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDSEFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

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127. The amino acid sequence according to claim 117, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:
- WLDQEWVQCEVYGRGCPSKK (SEQ ID NO:2227);
 - KWLDQEWAWVQCEVYGRGCPSKK (SEQ ID NO:1579);
 - KWLDQEWAWVQCEVYGRGCPS (SEQ ID NO:1580);
 - SLEEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
 - SLEEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
 - SLEEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
 - SLEEEWAQIECEVWGRGCPS (SEQ ID NO:1584).
128. The amino acid sequence according to claim 117, wherein the amino acid sequence is selected from the group consisting of sequences S432-S433 (SEQ ID NOS:2033-2036), S436-S445 (SEQ ID NOS:2037-2056), and S456 (SEQ ID NOS:2061-2062).
129. An amino acid sequence that is an insulin receptor antagonist, which comprises a subsequence that comprises a sequence that binds to Site 1 of insulin receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin receptor, wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 1 to Site 2, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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130. The amino acid sequence according to claim 129, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
131. The amino acid sequence according to claim 130, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
132. The amino acid sequence according to claim 130, wherein X_{63} is selected from the group consisting of leucine, isoleucine, methionine and valine; X_{70} and X_{74} are selected from group consisting of valine, isoleucine, leucine and methionine; X_{64} is selected from group consisting of aspartic acid and glutamic acid; X_{67} is tryptophan; and X_{75} is selected from group consisting of tyrosine and tryptophan.
133. The amino acid sequence according to claim 130, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
134. The amino acid sequence according to claim 130, wherein the Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$ is WLDQEWAVVQCEVYGRGCP (SEQ ID NO:2056).

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135. The amino acid sequence according to claim 130, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NO:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
136. The amino acid sequence according to claim 130, wherein the Formula 6 sequence is selected from the group consisting of sequences SEQ ID NO:926-1061 (Figures 3A-3E); SEQ ID NO:1244-1253 (Figure 9A); and SEQ ID NO:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
137. The amino acid sequence according to claim 130, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805, 1556, and 1806-1807), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).

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138. The amino acid sequence according to claim 130, wherein the Formula 6 sequence is selected from the group consisting of sequences S256 (SEQ ID NO:1893), S263 (SEQ ID NO:1899), S266 (SEQ ID NO:1902), S284-285 (SEQ ID NOS:1909-1910), S515 (SEQ ID NO:2102), and RB426 (SEQ ID NO:2158).
139. The amino acid sequence according to claim 130, wherein the Formula 1 sequence is selected from the group consisting of sequences
- H2C/D117: FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADEDFYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFDRLS (SEQ ID NO:1562);
GQLDEDFYEWFDRLS (SEQ ID NO:1563);
GQLDEDFYAWFDRLS (SEQ ID NO:1564);
GFMDSEFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDSEFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).

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140. The amino acid sequence according to claim 130, wherein the Formula 6 sequence is a D8 sequence selected from the group consisting of:
- WLDQEWVQCEVYGRGCPSKK (SEQ ID NO:2227);
KWLDQEWAWVQCEVYGRGCPSKK (SEQ ID NO:1579);
KWLDQEWAWVQCEVYGRGCPS (SEQ ID NO:1580);
SLEEWAQIQCEIYGRGCRY (SEQ ID NO:1581);
SLEEWAQIQCEIWGRGCRY (SEQ ID NO:1582);
SLEEWAQIECEVYGRGCPS (SEQ ID NO:1583); and
SLEEWAQIECEVWGRGCPS (SEQ ID NO:1584).
141. The amino acid sequence according to claim 130, wherein the amino acid sequence is selected from the group consisting of sequences 537-538 (SEQ ID NOS:2114-2115).
142. The amino acid sequence according to claim 130, wherein the amino acid sequence is selected from the group consisting of sequences S425 (SEQ ID NO:2031), S454 (SEQ ID NOS:2058-2059), S459 (SEQ ID NO:2065), and RB537-RB538 (SEQ ID NOS:2197-2198).
143. The amino acid sequence according to claim 129, wherein the Site 1 sequences consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{22} , X_{25} , X_{26} , X_{28} , X_{29} , X_{30} , X_{33} , X_{34} , X_{35} , X_{37} , X_{38} , X_{40} and X_{41} are any amino acid; X_{23} is any hydrophobic amino acid; X_{27} is a polar amino acid; X_{31} is an aromatic amino acid; X_{32} is a small amino acid; and wherein at least one cysteine is located at positions X_{24} through X_{27} and one at X_{39} or X_{40} .

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144. The amino acid sequence according to claim 143, wherein X_1 , X_2 , and X_5 are selected from the group consisting of phenylalanine and tyrosine, X_3 is selected from the group consisting of aspartic acid, glutamic acid, glycine and serine, and X_4 is selected from group consisting of tryptophan, tyrosine and phenylalanine.
145. The amino acid sequence according to claim 143, wherein X_{24} and X_{39} are cysteines, X_{23} is selected from leucine, isoleucine, methionine and valine; X_{27} is selected from glutamic acid, aspartic acid, asparagine, and glutamine; X_{31} is tryptophan, X_{32} is glycine; and X_{36} is any aromatic amino acid.
146. The amino acid sequence according to claim 143, wherein the Formula 1 sequence $X_1X_2X_3X_4X_5$ is FYDWF (SEQ ID NO:1554).
147. The amino acid sequence according to claim 143, wherein the Formula 4 sequence $X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}X_{28}X_{29}X_{30}X_{31}X_{32}X_{33}X_{34}X_{35}X_{36}X_{37}X_{38}X_{39}X_{40}X_{41}$ is HLCVLEELFWGASLFGYCSG (SEQ ID NO:1576).
148. The amino acid sequence according to claim 143, wherein the Formula 1 sequence is selected from the group consisting of sequences SEQ ID NOS:1-712 (Figures 1A-1O); SEQ ID NOS:1221-1243 (Figure 8); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).
149. The amino acid sequence according to claim 143, wherein the Formula 4 sequence is selected from the group consisting of sequences SEQ ID NOS:713-925 (Figures 2A-2E); SEQ ID NOS:1254-1261 (Figure 9B); and SEQ ID NOS:1596, 1718-1719, 1556, 1560, and 1720-1776 (Table 2).

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150. The amino acid sequence according to claim 143, wherein the Formula 1 sequence is selected from the group consisting of sequences S105-S116 (SEQ ID NOS:1791-1805), S131 (SEQ ID NO:1820), S137 (SEQ ID NO:1821), S158 (SEQ ID NO:1780), S165-S168 (SEQ ID NOS:1554, and 1824-1826), S171 (SEQ ID NO:1831), S175-S176 (SEQ ID NOS:1560 and 1836), S179-S184 (SEQ ID NOS:1839-1844), S214-216 (SEQ ID NOS:1845-1847), S219-223 (SEQ ID NOS:1852-1856), S227 (SEQ ID NO:1858), S234-245 (SEQ ID NOS:1869-1880), S248-S251 (SEQ ID NOS:1883-1886), S264-S265 (SEQ ID NOS:1900-1901), S268 (SEQ ID NO:1903), S278 (SEQ ID NO:1905), S287 (SEQ ID NO:1911), S294-S295 (SEQ ID NOS:1922-1923), S315 (SEQ ID NO:1937), S319-322 (SEQ ID NOS:1940-1943), S326 (SEQ ID NO:1600), S342 (SEQ ID NO:1962), S365-S366 (SEQ ID NOS:1987-1988), S371-S373 (SEQ ID NOS:1558, and 1990-1991), S386-S403 (SEQ ID NOS:1559, 2005-2007, 1794, 2008-2009, 1788, 1787, 1789, 2010-2011, 1791, and 2012-2014), RB437 (SEQ ID NO:2164), RB502 (SEQ ID NO:2170), RB452 (SEQ ID NO:2173), RB513 (SEQ ID NO:2176), RB464 (SEQ ID NO:2179), RB596 (SEQ ID NO:2202), RB569 (SEQ ID NO:2203), and RB570 (SEQ ID NO:2204).
151. The amino acid sequence according to claim 143, wherein the Formula 4 sequence is selected from the group consisting of sequences S262 (SEQ ID NO:1898), S282-S283 (SEQ ID NOS:1907-1908), S331 (SEQ ID NO:1949), RB505M (SEQ ID NO:2160), RB446 (SEQ ID NO:2180), and RB505 (SEQ ID NO:2191).
152. The amino acid sequence according to claim 143, wherein the Formula 4 sequence is selected from the group consisting of sequences RB517M (SEQ ID NO:2161), RB515 (SEQ ID NO:2162), and RB510 (SEQ ID NO:2163).

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153. The amino acid sequence according to claim 143, wherein the Formula 1 sequence is selected from the group consisting of sequences
- H2C/D117: FHENFYDWFVRQVSKK (SEQ ID NO:1556);
FHENFYDWFVRQVS (SEQ ID NO:1557);
RP9: GSLDESFYDWFERQLGKK (SEQ ID NO:1558);
GSLDESFYDWFERQLG (SEQ ID NO:1559);
GLADED FYEWFERQLR (SEQ ID NO:1561);
GLADELFYEWFD RQLS (SEQ ID NO:1562);
GQLDEDFYEWFD RQLS (SEQ ID NO:1563);
GQLDEDFYAWFD RQLS (SEQ ID NO:1564);
GFMDESFYEWFERQLR (SEQ ID NO:1565);
GFWDESFYAWFERQLR (SEQ ID NO:1566);
GFMDESFYAWFERQLR (SEQ ID NO:1567);
GFWDESFYEWFERQLR (SEQ ID NO:1568);
RP15: SQAGSAFYAWFDQVLRTV (SEQ ID NO:2057); and
S175: GRVDWLQRNANFYDWFVAELG (SEQ ID NO:1560).
154. The amino acid sequence according to claim 143, wherein the amino acid sequence is selected from the group consisting of sequences 431-433 (SEQ ID NOS:2135-2137).
155. The amino acid sequence according to claim 143, wherein the amino acid sequence is selected from the group consisting of sequences RB431-RB433 (SEQ ID NOS:2184, 2186, and 2188).
156. A pharmaceutical composition comprising the amino acid sequence according to claim 79, and a physiologically acceptable carrier, excipient or diluent.
157. A pharmaceutical composition comprising the amino acid sequence according to claim 106, and a physiologically acceptable carrier, excipient or diluent.

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158. A pharmaceutical composition comprising an amino acid sequence according to claim 116, a physiologically acceptable carrier, excipient or diluent.
159. A pharmaceutical composition comprising the amino acid sequence according to claim 129, and a physiologically acceptable carrier, excipient or diluent.
160. A method of treating diabetes comprising administering to an individual in need of treatment a therapeutically effective amount of the pharmaceutical composition according to claim 156, thereby treating the diabetes.
161. A method of treating diabetes comprising administering to an individual in need of treatment a therapeutically effective amount of the pharmaceutical composition according to claim 157, thereby treating the diabetes.
162. A method of treating diabetes comprising administering to an individual in need of treatment a therapeutically effective amount of the pharmaceutical composition according to claim 158, thereby treating the diabetes.
163. A method of treating insulin shock comprising administering to an individual in need of treatment a therapeutically effective amount of the pharmaceutical composition according to claim 159, thereby treating the insulin shock.
164. A method of identifying an insulin agonist comprising:
 - 1) producing a secondary library comprising peptides derived from the amino acid sequence according to claim 79;
 - 2) screening the library peptides for binding to insulin receptor; and
 - 3) screening the insulin-binding peptides from (2) for agonist activity for insulin receptor, wherein agonist activity indicates identification of an insulin receptor agonist.

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165. A method of identifying an insulin agonist comprising:
- 1) producing a secondary library comprising peptides derived from the amino acid sequence according to claim 106;
 - 2) screening the library peptides for binding to insulin receptor; and
 - 3) screening the insulin-binding peptides from (2) for agonist activity for insulin receptor, wherein agonist activity indicates identification of an insulin receptor agonist.
166. A method of identifying an insulin agonist comprising:
- 1) producing a secondary library comprising peptides derived from the amino acid sequence according to claim 116;
 - 2) screening the library peptides for binding to insulin receptor; and
 - 3) screening the insulin-binding peptides from (2) for agonist activity for insulin receptor, wherein agonist activity indicates identification of an insulin receptor agonist.
167. A method of identifying an insulin antagonist comprising:
- 1) producing a secondary library comprising peptides derived from the amino acid sequence according to claim 129;
 - 2) screening the library peptides for binding to insulin receptor; and
 - 3) screening the insulin-binding peptides from (2) for antagonist activity for insulin receptor, wherein antagonist activity indicates identification of an insulin receptor antagonist.
168. A method of increasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence comprising a sequence selected from the group consisting of SLEEEWAQVECEVYGRGCPSGSLDESFYDWFERQLG (S519; SEQ ID NO:2033) and SIEEEWAQIKCDVWGRGCP PGLLDESFYHWFDRQLR (S520; SEQ ID NO:2034), and a physiologically acceptable carrier, excipient, or diluent, in amount sufficient to increase insulin activity.

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169. An amino acid sequence that is an insulin receptor agonist, which comprises a sequence selected from the group consisting of SLEEEWAQVECEVYGRGCPSGSLDESFYDW FERQLG (S519; SEQ ID NO:2033) and SIEEEWAQIKCDVWGRGCPPGLLDESFYHWFDRLR (S520; SEQ ID NO:2034).
170. A pharmaceutical composition comprising the amino acid sequence according to claim 169, and a physiologically acceptable carrier, excipient or diluent.
171. A method of treating diabetes comprising administering to an individual in need of treatment a therapeutically effective amount of the pharmaceutical composition according to claim 170, thereby treating the diabetes.
172. A method of identifying an insulin agonist comprising:
- 1) producing a secondary library comprising peptides derived from the amino acid sequence according to claim 169;
 - 2) screening the library peptides for binding to insulin receptor; and
 - 3) screening the insulin-binding peptides from (2) for agonist activity for insulin receptor, wherein agonist activity indicates identification of an insulin receptor agonist.

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173. A method of increasing insulin-like growth factor receptor activity in mammalian cells comprising administering to said cells an amino acid sequence in an amount sufficient to increase insulin-like growth factor activity, wherein the amino acid sequence comprises a subsequence that comprises a sequence that binds to Site 1 of insulin-like growth factor receptor and a subsequence that comprises a sequence that binds to Site 2 of insulin-like growth factor receptor, and wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 2 to Site 1, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.
174. The method according to claim 173, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
175. An amino acid sequence that is an insulin-like growth factor receptor agonist, which comprises a subsequence that comprises a sequence that binds to Site 1 of the insulin-like growth factor receptor and a subsequence that comprises a sequence that binds to Site 2 of the insulin-like growth factor receptor, wherein the subsequences are linked C-terminus to N-terminus and the subsequences are oriented Site 2 to Site 1, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.

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176. The amino acid sequence of claim 175, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$ and the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, and wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid, and wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.
177. An amino acid sequence that binds to insulin-like growth factor receptor, which comprises a sequence selected from the group consisting of a sequence that binds to Site 1 of the insulin-like growth factor receptor and a sequence that binds to Site 2 of the insulin-like growth factor receptor, with the proviso that the amino acid sequence is not insulin, insulin-like growth factor, or fragments thereof.
178. The amino acid sequence of claim 177, wherein the Site 1 sequence consists essentially of a Formula 1 sequence $X_1X_2X_3X_4X_5$, wherein X_1 , X_2 , X_4 , and X_5 are aromatic amino acids, and X_3 is any polar amino acid.
179. The amino acid sequence of claim 177, wherein the Site 1 sequence consists essentially of a Formula 2 sequence $X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}$, wherein X_6 and X_7 are aromatic amino acids, X_8 , X_9 , X_{11} , and X_{12} are any amino acid, and X_{10} and X_{13} are hydrophobic amino acids.
180. The amino acid sequence of claim 177, wherein the Site 2 sequence consists essentially of a Formula 6 sequence $X_{62} X_{63} X_{64} X_{65} X_{66} X_{67} X_{68} X_{69} X_{70} X_{71} X_{72} X_{73} X_{74} X_{75} X_{76} X_{77} X_{78} X_{79} X_{80} X_{81}$, wherein X_{62} , X_{65} , X_{66} , X_{68} , X_{69} , X_{71} , X_{73} , X_{76} , X_{77} , X_{78} , X_{80} and X_{81} are any amino acid; X_{63} , X_{70} , and X_{74} are hydrophobic amino acids; X_{64} is a polar amino acid; X_{67} and X_{75} are aromatic amino acids; and X_{72} and X_{79} are cysteines.

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181. The method according to claim 29, wherein the amino acid sequence is selected from the group consisting of: S527-S546; S549, D551-S591; S594-S624; S626-S639; and S641-S648.
182. The method according to claim 181, wherein the amino acid sequence is selected from the group consisting of S557 and S597.
183. A method of increasing insulin receptor activity in mammalian cells comprising administering to said cells an amino acid sequence selected from the group consisting of: S527-S546; S549, D551-S591; S594-S624; S626-S639; and S641-S648 and a physiologically acceptable carrier, excipient, or diluent, in an amount sufficient to increase insulin receptor activity.
184. The method according to claim 183, wherein the amino acid sequence is selected from the group consisting of S557 and S597.
185. An amino acid sequence that is an insulin receptor agonist, which comprises a sequence selected from the group consisting of: S527-S546; S549, D551-S591; S594-S624; S626-S639; and S641-S648.
186. The sequence according to claim 185, wherein the sequence is selected from the group consisting of S557 and S597.
187. A method of treating diabetes, said method comprising administering to a patient in need of such treatment (i) a first amount of a first compound selected from the group consisting of: peptides S519, S520; S524, S527-S546, S549, D551-S591, S594-S624, S626-S639, and S641-S648 and (ii) a second amount of a second compound comprising a long-acting insulin analogue, wherein the first and second amounts together are effective for treating said diabetes.
188. The method according to claim 187, wherein said first compound is selected from the group consisting of: S557 and S597.

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189. The method according to claim 187, wherein said long-acting insulin analogue is selected from the group consisting of LysB29(-myristoyl)des(B30) human insulin, LysB29(-tetradecanoyl)des(B30) human insulin, and B29-N -(N-lithocolyl- -glutamyl)-des(B30) human insulin

Clone	Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
R40-3-40B2-IR		XXXXXXXXXXXXXXXXXXXXXXXXXXXXX IRDMHYVWQDRDRIYINGVRQWYISDRYNPGSAFYRWFD	--	--	--	--	--	
R40-4-40B12-IR		RMGLQALAHYRKSA GPIFLSSGSVIKSGEDFFYAWFRLQ	40.3	9.0	2.0	4.5	0.2	
R40-4-40G11-IR		MPVSLFRRVWDYRDGEHETLES HYVVPQAALDRLEFSWFS	60.4	12.9	2.0	6.5	0.2	
			52.6	37.5	2.0	18.8	0.1	

FIG. 1A

Clone	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF ₃ R	IGFR/IR	IR/IGFR
Design	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--
R40-3-D5-IGFR	PLYGGGIHLYPGTMGVYPGFPQRQKVLGDADKNFYDWEM	--	--	--	--
R40-3-A6-IGFR	YRGLVLGRISDGAGKVASEPPARIGQKVFVAFNFDWVF	--	--	--	--
R40-X-R35-IGFR	SGCCRLGLRLWMFIVVGWSGALVCQSAASAAGFYDWVF	--	--	--	--

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
	XXXXXXXXXXXXXXXXXXXX	--	--	--	--	--	
R20 α -3-20D3-IR	IGGQGHQDGNFYDFWFEALA	46.3	36.2	7.0	5.2	0.2	
R20 α -3-20F1-IR	VFWNCRSQQLDFYEWFEQAA	49.0	26.0	2.8	9.3	0.1	
R20 α -3-20H1-IR	RVAGAI SAPGLVSNKQDGLFYSWFRE	45.6	35.3	3.3	10.7	0.1	
R20 α -3-20D1-IR	VLQARHGCDSDVDCFYEWFA	50.8	37.5	3.0	12.5	0.1	
R20 β -4-B12-IR	GAFYRWFHEALVGSERVPDV	41.9	2.9	5.7	0.5	2.0	
R20 β -4-H3-IR	HEAFYDWFSAVDGGYELMG	13.9	5.8	2.4	2.4	0.4	
R20 β -4-D10-2-IR	RIGGGWARSEGFEWFEVREL	21.5	7.3	2.9	2.5	0.4	
R20 β -4-C8-IR	LPAGGA?GFA?RGFEWFES	44.9	31.1	9.6	3.2	0.3	
R20 β -4-E7-IR	GHSWALVRHVDRLFYEWFDL	45.0	18.8	5.9	3.2	0.3	
R20 β -4-E7-2-IR	LGTSAGQGVGHRAFYQWFQS	45.0	18.8	5.9	3.2	0.3	
R20 β -4-G3-IR	RGGTFYEWFEFESALRKHGAG	38.6	7.5	2.0	3.8	0.3	
R20 β -4-H6-IR	NSSGQQVVGLTFYSWFEASQV	14.8	7.6	2.0	3.8	0.3	
R20 β -4-G11-IR	FYGWFSRQLSLTPRDDWGLP	39.4	7.5	1.9	3.9	0.3	
R20 β -4-G8-IR	RMFYENFWFSQMGAGPTEGSA	41.2	15.1	3.4	4.4	0.2	
R20 β -4-H9-IR	IGGQGHQDGNFYDNFVEALA	43.1	8.8	2.0	4.4	0.2	
R20 β -4-H8-IR	RDKPTDQEEQNWSFYEWFRH	47.9	43.7	9.3	4.7	0.2	
R20 β -4-B8-IR	WSALLSVMDTGFYAWFDDAV	44.0	40.1	8.4	4.8	0.2	
R20 β -4-E2-IR	SRDQTNFTFNSAGFYGWFER	16.3	13.9	2.4	5.8	0.2	
R20 β -4-F4-IR	GVGTLTMSSDAFYTWFFV	15.3	5.9	1.0	5.9	0.2	
R20 β -4-A8-IR	IGGSFVEFYGWFNQDV	43.3	36.0	6.0	6.0	0.2	
R20 β -4-C4-IR	DIGSDGHGRRWDSFYRWFEEM	17.3	26.8	4.3	6.2	0.2	
R20 β -4-D7-IR	VLQARHGCDSDVDCFYEWFA	44.8	36.2	5.6	6.5	0.2	
R20 β -4-D2-IR	DPERMQSDVGFYEWFEAAVG	31.2	29.4	2.9	10.1	0.1	

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FIG. 1C

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF ₃ R	IGFR/IR	IR/IGFR
R20-4-B9-IGFR	XXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--
R20-4-F8-IGFR	DPERMQSDVGFYEWFRAAVG	40.1	16.6	--	--
R20-4-G12-IGFR	DIGSDGHGRRWDSFYRWFEM	39.2	13.9	--	--
R20-4-D10-IGFR	PFYQWFLDQSVGSGRGGGLR	36.7	8.0	--	--
	AVAPLSVRGRDSGFYSWFSS	40.2	4.1	--	--

FIG. 1D

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR
A6S-3-E12-IR	XXXXXXXXXXNFYDFVXXXX	26.2	1.3	8.0	0.2
A6S-2-C1-IR	GRVDWLQRNANFYDFVAELG	41.2	1.3	7.0	0.2
A6S-1-A7-IR	RMVFSTGAPQNFYDFVQEW	47.2	2.3	11.1	0.2
A6S-2-C8-IR	HHTQGLQVQRNFYDFVNELR	44.9	1.5	5.5	0.3
A6S-3-E10-IR	MHRMQHDGTSNFYDFVFLQWA	46.9	1.6	5.0	0.3
A6S-2-D5-IR	AMHVVAQGGPNFYDFVRELR	31.9	1.2	3.7	0.3
A6S-1-B2-IR	AIQMNGNLAFNFYDFVRELT	31.6	1.8	5.3	0.3
A6S-1-A4-IR	TDRKSVQEPNRFYDFVFWAAR	43.3	3.6	9.2	0.4
A6S-4-G3-IR	PHGHRGFAQSNFYDFVFTQEE	31.3	2.3	5.1	0.5
A6S-4-H8-IR	RLASASVPGQNFYDFVFDQLL	11.5	1.7	3.6	0.5
A6S-3-E11-IR	RQSEFSTLNSNFYDFVRELE	26.3	2.3	4.4	0.5
A6S-1-A1-IR	GQAQLSIRDVNFYDFVQQLV	36.9	3.7	6.5	0.6
A6S-2-C9-IR	MSEPAVGNGNFYDFVFAQLF	43.6	1.3	2.3	0.6
A6S-2-C4-IR	VGTGRARLDRNFYDFVFGQYS	34.5	5.6	9.6	0.6
A6S-4-H10-IR	SREAVQKRANFYDFVQQLS	39.2	4.4	6.9	0.6
A6S-4-G7-IR	LAQFAGSRNQNFYDFVEQLG	19.1	1.4	2.2	0.6
A6S-4-H2-IR	GQEYFDQMGLNFYDFVRELD	25.5	2.6	3.9	0.7
A6S-2-C3-IR	RQPSQPPHGSNFYDFVEAIN	31.1	1.6	2.4	0.7
A6S-2-C11-IR	LMQSLGSGSTNFYDFVQQMV	20.9	3.3	4.6	0.7
A6S-3-F3-IR	DQQRACDGTNFYDFVVCQLS	37.1	3.0	4.2	0.7
A6S-3-E5-IR	LDGTKACQVRNFYDFVVCQTE	31.6	2.5	3.5	0.7
A6S-1-B7-IR	PEARRTVVHSNFYDFVFAQLS	49.2	1.6	2.3	0.7
A6S-3-E7-IR	PWMLSVGIQDNFYDFVGLDS	37.2	5.0	6.3	0.8
A6S-4-G6-IR	ASHQRGSSDNFYDFVFAQMR	16.8	3.1	4.0	0.8
A6S-2-C2-IR	TLEREGEFSGNFYDFVEQLH	29.7	2.4	3.1	0.8
A6S-3-F1-IR	DRQSIGSVHGDYDFVFSALG	29.7	2.3	3.0	0.8
A6S-2-C5-IR	DWDKLGSLSENFYDFVFDQLA	42.9	6.1	7.0	0.9
A6S-3-E4-IR	VRVVLNQSGRNFYDFVFIQLE	20.9	2.1	2.3	0.9
	MASWQSRTPDNFYDFVRELS				

FIG. 1E-1

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFsR/IR	IR/IGFsR	IR/IGFsR
	XXXXXXXXXXNFYDWFVXXXX	--	--	--	--	--	--
A6S-3-E9-IR	TTCHPRGEDCNFYDWFVQLQR	36.6	9.0	8.9	1.0	1.0	1.0
A6S-3-E1-IR	VRGNDSVLRANFYDWFVDQLS	36.7	6.8	6.9	1.0	1.0	1.0
A6S-4-H12-IR	TPRSQVRSRDNFYDWFVYQLA	46.3	6.1	5.8	1.1	1.1	1.0
A6S-2-D3-IR	ESLTGSRPDRNFYDWFVQQT	37.0	5.3	5.1	1.0	1.0	1.0
A6S-3-E8-IR	PQSLTEVRTGNFYDWFVQLH	42.7	5.2	5.1	1.0	1.0	1.0
A6S-1-A12-IR	DVGMGRVKEITNFYDWFVRQLI	39.7	2.1	2.1	1.0	1.0	1.0
A6S-4-H3-IR	GADDIRSLTNFYDWFVNQLS	18.6	3.1	2.9	1.1	1.1	0.9
A6S-3-F7-IR	GVSIOAGYKTNFYDWFVEAVR	46.2	2.3	2.1	1.1	1.1	0.9
A6S-2-D8-IR	VGEHRQMSVGNFYDWFVMQIA	31.2	2.0	1.7	1.2	1.2	0.9
A6S-3-F10-IR	GSSLGRSGPGNFYDWFVDQLE	39.0	5.9	4.5	1.3	1.3	0.8
A6S-4-G11-IR	HRQQDVVRQGNFYDWFVQALE	44.8	4.3	3.3	1.3	1.3	0.8
A6S-2-D2-IR	QDTFLTAREGNFYDWFIRALE	33.5	3.6	2.7	1.3	1.3	0.8
A6S-4-G8-IR	EAIMREEGQANFYDWFVRQLE	11.1	2.5	1.9	1.3	1.3	0.8
A6S-4-H6-IR	VCDVSTGGTNFYDWFVCQVG	22.4	2.4	1.9	1.3	1.3	0.8
A6S-2-D10-IR	PQPRASSTPLNFYDWFVQATG	41.3	2.1	1.7	1.2	1.2	0.8
A6S-3-F4-IR	GVSRGSGGDPNFYDWFVMQLR	37.0	13.5	9.9	1.4	1.4	0.7
A6S-4-G9-IR	GPGRHDSSRGNFYDWFVEQLA	36.2	11.8	7.8	1.5	1.5	0.7
A6S-3-F5-IR	ERFALEVQGSNFYDWFVRQVI	48.1	7.2	4.8	1.5	1.5	0.7
A6S-4-H1-IR	NLKSSATVGGNFYDWFVEQL	18.3	3.6	2.6	1.4	1.4	0.7
A6S-3-F6-IR	MEGPPAGGPLNFYDWFVAQVD	18.7	2.9	1.9	1.5	1.5	0.7
A6S-3-F11-IR	RLDVAGHRGGNFYDWFVKQLH	33.8	2.0	1.4	1.4	1.4	0.7
A6S-2-C6-IR	PWSDHEALNQNFYDWFVSQVL	46.7	19.2	12.1	1.6	1.6	0.6
A6S-4-G4-IR	EDRLNGESTNFYDWFVRQLA	36.9	18.2	10.7	1.7	1.7	0.6
A6S-4-G12-IR	GKLVASTLDDNFYDWFVRQLS	32.8	12.8	7.9	1.6	1.6	0.6
A6S-2-D7-IR	SGPVVQTQNGNFYDWFVHQLR	33.2	12.0	7.1	1.7	1.7	0.6
A6S-4-G10-IR	VDRAGPAGSDNFYDWFVAQLD	33.9	10.8	6.8	1.6	1.6	0.6
A6S-3-F9-IR	SLGRNDRPDENFYDWFVSQVQ	44.3	9.6	5.7	1.7	1.7	0.6
A6S-3-F2-IR	RVMATANAPMNFYDWFVVQLQ	23.2	4.3	2.5	1.7	1.7	0.6

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FIG. 1E-2

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	--
A6S-4-G1-IR	XXXXXXXXXXXXNFYDWFVXXXX	36.2	31.8	15.7	2.0	0.5	0.5
A6S-1-A3-IR	NGVERAGTGDNFYDWFVAQLH	39.9	12.6	6.0	2.1	0.5	0.5
A6S-3-F12-IR	PFAGKGDKTGNFYDWFVSLTG	41.4	7.4	4.0	1.9	0.5	0.5
A6S-4-G2-IR	GMPQEYMDQVNFYDWFVAQVD	26.7	7.0	3.5	2.0	0.5	0.5
A6S-1-B1-IR	MGTPAVGDGANFYDWFVRQLG	30.6	3.7	1.9	1.9	0.5	0.5
A6S-2-D11-IR	SKCKAWYGANNFYDWFVWQVD	48.4	37.4	13.5	2.8	0.4	0.4
A6S-2-D1-IR	EAASLGSQDRNFYDWFVRQVV	37.8	30.6	12.0	2.6	0.4	0.4
A6S-3-E2-IR	VERSASSQDGNFYDWFVQIR	33.1	24.7	9.8	2.5	0.4	0.4
	TSEVQRRSQDNFYDWFVAQVA						

FIG. 1E-3

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF ₅ R	IGFR/IR	IR/IGFR
A6S-4-E4-IGFR	XXXXXXXXXXXXNFYDFVXXXX	--	--	--	--
A6S-2-D2-IGFR	ERSAAGFREGNFYDFVQAQVN	27	32	--	--
A6S-2-F2-IGFR	RAERGSMDNSFYDFVQQLP	36	30	--	--
A6S-4-F3-IGFR	LAMSVASRPANFYDFVQAQIV	35	30	--	--
A6S-4-G4-IGFR	HNSSPMRTGNFYDFVQELR	26	30	--	--
A6S-4-G3-IGFR	SALSGPVQPINFYDFVVTGM	26	30	--	--
A6S-2-H2-IGFR	GAQAIREIHNFYDFVQAQVT	21	29	--	--
A6S-2-E3-IGFR	RGQRESDSGTNFYDFVGAIR	40	28	--	--
A6S-4-C6-IGFR	VQEGLSGMEGNFYDFVDQLF	36	28	--	--
A6S-4-F5-IGFR	RLDRSSTSGVNFYDFVQAQVG	25	28	--	--
A6S-4-H3-IGFR	GSQHSGREPHNFYDFVQAQVG	24	28	--	--
A6S-4-H4-IGFR	GRGQRHETTNFYDFVRELQ	20	28	--	--
A6S-2-H1-IGFR	PRMVEKPSEDNFYDFVTQLS	20	28	--	--
A6S-4-E6-IGFR	RVGIQVDPHTNFYDFVVIQLT	42	27	--	--
A6S-4-B6-IGFR	RSSGGLSQGNFYDFVFSQLE	24	26	--	--
A6S-4-D2-IGFR	SDARQAGLQENFYDFVFSQVR	23	26	--	--
A6S-4-G5-IGFR	PPYRSSRLGENFYDFVFMQVR	19	26	--	--
A6S-2-A3-IGFR	QEVTRTRDDKNFYDFVFSQIF	18	26	--	--
A6S-4-E2-IGFR	SRAPYGSTAGNFYDFVQAVS	37	25	--	--
A6S-4-G6-IGFR	?DQSVSSKGNFYDFVQQMT	25	25	--	--
A6S-4-G2-IGFR	RLMGGIAEPQNFYDFVREVA	20	25	--	--
A6S-4-D6-IGFR	SAGHMPRESNFYDFVDQVV	25	24	--	--
A6S-4-F4-IGFR	LGAETWDGINFYDFVFKQVS	22	24	--	--
A6S-4-C3-IGFR	VGHSGVPPYPNFYDFVFMQVS	22	24	--	--
A6S-4-H5-IGFR	VTMLDKGAQDNFYDFVREVA	21	24	--	--
A6S-4-H6-IGFR	HHSPGNEHGYNFYDFVLIQVA	19	24	--	--
A6S-4-F6-IGFR	GSIAQLIMRANFYDFVVEQTN	18	24	--	--
A6S-3-H1-IGFR	LKGSSQPLSVNFYDFVQQIK	17	24	--	--
	PASNKNLAENFYDFVQQTTR	30	23	--	--

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FIG. 1F--1

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Ratios over Background		Comparisons				
Clone	Design	Sequence	E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
A6S-4-A6-IGFR		XXXXXXXXXXNFYDFVXXXX	--	--	--	--
A6S-4-E3-IGFR		HVEHMAVG ^{DN} GFYDFV ^{VQ} LR	21	23	--	--
A6S-4-D3-IGFR		RGMTGMVGRGNFYDFV ^{GQ} LR	21	23	--	--
A6S-3-E10-IGFR		GLRSEQGNRLNFYDFV ^{QA} IA	20	23	--	--
A6S-4-D1-IGFR		RVREKLPRPENFYDFV ^{NQ} IH	23	22	--	--
A6S-4-B2-IGFR		SNPSRQDASVNFYDFV ^{RE} VA	22	22	--	--
A6S-4-A2-IGFR		QSV ^{DL} SRPDSNFYDFV ^{EV} LS	21	22	--	--
A6S-4-A5-IGFR		IGGQGHQDGNFYDFV ^{EA} LA	20	22	--	--
A6S-4-C1-IGFR		VEVQRH ^{IR} KDKNFYDFV ^{KQ} ID	19	22	--	--
A6S-4-B1-IGFR		CWARPCGDAANFYDFV ^Q QAS	16	22	--	--
A6S-4-B4-IGFR		RHERGKEGPNFYDFV ^{SQ} VV	19	21	--	--
A6S-4-D4-IGFR		ERSPRPALASNFYDFV ^Q QV	19	21	--	--
A6S-3-F8-IGFR		IARMRETFQPNFYDFV ^{DQ} LA	18	21	--	--
A6S-3-H9-IGFR		GRGQGLKRP ^{DN} FYDFV ^{AA} AK	25	20	--	--
A6S-3-G2-IGFR		YSIEVQDWNENFYDFV ^{SQ} LG	23	20	--	--
A6S-4-H2-IGFR		TWMWEERKQDNFYDFV ^{GQ} LK	21	20	--	--
A6S-4-A3-IGFR		VTFTSAVFHENFYDFV ^{FR} QVS	19	20	--	--
A6S-3-G10-IGFR		LAINDLVTHKNFYDFV ^{DQ} LR	18	20	--	--
A6S-3-E5-IGFR		GAVGLAEAGPNFYDFV ^{SQ} VQ	24	19	--	--
A6S-3-H2-IGFR		RYRGERHDGRNFYDFV ^{EQ} VN	21	19	--	--
A6S-3-G3-IGFR		QGAEGRLSEGNFYDFV ^Q AVS	21	19	--	--
A6S-4-H1-IGFR		PRLHMGSDMGDFYDFV ^{VQ} IA	21	18	--	--
A6S-4-G1-IGFR		IVAGARHSEVNFYDFV ^{VI} QVR	18	18	--	--
A6S-4-A1-IGFR		AELVGAGVRGNFYDFV ^{DQ} LV	16	16	--	--
A6S-2-F1-IGFR		DSSRLWLGERNFYDFV ^{QA} IS	17	12	--	--
A6S-2-G1-IGFR		VGQVGRYVRSNFYDFV ^Q QAM	30	8	--	--
A6S-1-C5-IGFR		RPQLVESGSKNFYDFV ^Q WVR	30	8	--	--
A6S-2-B2-IGFR		RIHNQTERGGNFYDFV ^{QH} QLV	27	7	--	--
		EMYGDTSERVNFYDFV ^{SAL} Q	30	5	--	--

FIG. 1F-2

Ratios over Background		Sequence	Comparisons				
Clone	Design		E-Tag	IGF8R	IR	IGFR/IR	IR/IGFR
A6S-1-D5-IGFR		XXXXXXXXXXXXNFYDWFVXXXXX	--	--	--	--	--
A6S-1-A2-IGFR		RVGSGMEDLGNFYDWFVRQAQ	25	5	--	--	--
A6S-3-E6-IGFR		KDPVTVSQGRNFYDWFVVQIQ	20	5	--	--	--
A6S-1-G3-IGFR		DARDHGVVWMSNFYDWFVAQVS	20	5	--	--	--
A6S-3-G4-IGFR		VATVHVGGGMNFYDWFVAQVG	19	5	--	--	--
A6S-3-H8-IGFR		CADPGACSSLNFYDWFVQMRG	21	4	--	--	--
A6S-3-E3-IGFR		NPTSVQQYGVNFYDWFVNVL	20	4	--	--	9/122
A6S-3-D9-IGFR		RPSLPEVRPGNFYDWFVQSVR	19	4	--	--	--
A6S-2-A1-IGFR		SLQGADEFQGNFYDWFVSELA	17	4	--	--	--
A6S-1-H4-IGFR		LSSRGRVTMRNFYDWFVAQVV	31	3	--	--	--
A6S-3-C1-IGFR		HKSWTTMSPLNFYDWFVAQVE	18	3	--	--	--
A6S-3-B10-IGFR		RPVIGGGGTRNFYDWFVAQMI	17	3	--	--	--
		YDQDPPYWGLNFYDWFVREVA	16	3	--	--	--

FIG. 1F-3

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-D1-IR		YRGMLVLGRISDGAGKVASEPPARIGQKVFAVNFYDWFV	19.0	.4.0	--	--	--
A6L-4-H7-IR		Q ¹ RGMLV ¹ RGRI ¹ SHGAGKIA ¹ YEPDCLGQKACAVNFYDWFV	22.6	19.8	26.5	0.7	1.3
A6L-4-H4-IR		Q ¹ RGMLL ¹ GRISD ¹ DAGKVASEPSARRGQKVFAFNFYDWFV	37.5	3.5	4.2	0.8	1.2
A6L-4-E4-IR		YRGILV ¹ LGRIS ¹ EGAGKVASEPAARIGQKVFAFNFYDWFV	38.5	21.1	25.8	0.8	1.2
A6L-4-G7-IR		Q ¹ RGMLAL ¹ GRISD ¹ GAGKVASEPPAGIGQKVFAFNFYDWFV	38.1	5.4	6.0	0.9	1.1
A6L-3-C3-IR		FRGRLV ¹ LGHFSD ¹ GAGKVGSEPAARIGQKVFDVNFYDWFV	38.6	16.2	18.5	0.9	1.1
A6L-3-B6-IR		YRGMLV ¹ LGRISD ¹ GAGKVASEPPARIGQEVFADNFYDWFV	34.7	21.8	23.1	0.9	1.1
A6L-4-G11-IR		YRGMLV ¹ LGRISD ¹ GAGEVASEPPARIGQEVFALNFYDWFV	33.1	27.8	30.3	0.9	1.1
A6L-4-G12-IR		VPWYAGSGSSSD ¹ GAGKVASEPPARIDQKVFAVNFYDWFV	27.6	2.0	2.0	1.0	1.0
A6L-3-A10-IR		YRGQLV ¹ LGRISY ¹ GAGKVGCDPPARIGQKDWAVNFYDWFV	32.0	2.3	2.3	1.0	1.0
A6L-4-E12-IR		Q ¹ RGLLV ¹ LGRFSD ¹ GAGNVASEPPAGIGQEVFPVNFYDWFV	21.1	2.4	2.4	1.0	1.0
A6L-4-E10-IR		Q ¹ RGMLV ¹ LGRISD ¹ GAGKVAEPPDCLGQKVCAVNFYDWFV	3.1	2.4	2.4	1.0	1.0
A6L-4-G8-IR		Q ¹ RGMRV ¹ LGRISD ¹ GAGKVASELPPRIGQKDFAVNFYDWFV	30.1	3.8	3.8	1.0	1.0
A6L-3-C12-IR		Q ¹ RGMLV ¹ LGSISD ¹ GAGKVAYEAPARIGQTVFAVNFYDWFV	37.9	4.7	4.7	1.0	1.0
A6L-4-H11-IR		Q ¹ QWCAGSGRIYD ¹ GACKVASEPPAHIGQEVFAVNFYDWFV	29.5	5.7	5.7	1.0	1.0
A6L-4-F10-IR		Q ¹ RGMLV ¹ LDRI ¹ SDGAGKVASGPPARIGQNVAVNFYDWFV	35.4	9.6	9.6	1.0	1.0
A6L-4-E9-IR		YRGMLV ¹ VGRISD ¹ GTGKVASQPPARIGQKVFAVNFYDWFV	31.6	10.5	10.5	1.0	1.0
A6L-4-H8-IR		YRGMLV ¹ LGRISD ¹ GAGKVASVPPAHIGQKVFAFNFYDWFV	39.8	12.9	12.9	1.0	1.0
A6L-3-A11-IR		Q ¹ HGMLV ¹ LGRVSVGAGKVPSEPPQARIGHKVFDFVNFYDWFV	38.2	14.6	14.6	1.0	1.0
A6L-4-F9-IR		YSGYAGSGSFS ¹ DGAGKVASEPPARISQEVLAADNFYDWFV	29.0	17.5	17.5	1.0	1.0
A6L-4-G2-IR		YRGMLV ¹ LGRISD ¹ GAGKVASEPPARIGQKVSAVNFYDWFV	35.7	18.4	18.4	1.0	1.0
A6L-4-E8-IR		YHGKLDLGRISVGVGKVASEPPARIGQKVFAFNFYDWFV	29.5	21.4	20.7	1.0	1.0
A6L-4-H10-IR		YRGQAGSGVGLTVAGKVASDPPARIGQKVFAFNFYDWFV	28.7	21.6	21.6	1.0	1.0
A6L-4-G9-IR		HRGMLV ¹ LGRIS ¹ EGAGNVDPPEPPARIGQNVFAGNFYDWFV	30.0	22.1	22.1	1.0	1.0
A6L-4-F7-IR		Q ¹ RGMPV ¹ LGRISD ¹ GAGKVSEPPARIA ¹ RKVFPVNFYDWFV	37.1	22.6	22.6	1.0	1.0
A6L-4-E11-IR		Q ¹ GGLLV ¹ TGRISD ¹ GAGKVASEPPGGIGQKVFAFNFYDWFV	28.6	23.6	24.4	1.0	1.0
		YPNWYGGSGTYLD ¹ GAGKVASEPPARIDQQVFAFNFYDWFV	38.4	26.5	26.5	1.0	1.0

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FIG. 1G-1

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsr	IR	IGFsr/IR	IR/IGFR	IR/IGFR
		YRGMLVLGRISDGAGKVA SEPPARIGQKVFAVNFYDWFV	19.0	.4.0	--	--	--	--
A6L-4-H9-IR		YRAMLVLRISDVAGIVDSEPPTRIGQKVFAVNFYDWFV	37.5	27.3	27.3	1.0	1.0	1.0
A6L-4-E1-IR		YRGMLVLGRISQAGNVA SEPSRIGQKVFAVNFYDWFV	35.4	32.6	31.4	1.0	1.0	1.0
A6L-3-A5-IR		YRGMLVLGRISDGAGKVDYEP PARIGQKVFAVNFYDWFV	38.3	34.6	35.5	1.0	1.0	1.0
A6L-4-G4-IR		YRGMLGLGISAGAGIVASEPPARVQKVFAVNFYDWFV	30.4	17.7	15.2	1.2	1.2	0.9
A6L-4-H2-IR		YRGILFQGRIPDGAGKVA SEPPTRIGERVFAVNFYDWFV	36.1	4.2	3.6	1.1	1.1	0.9
A6L-4-E6-IR		QGGMPVLGRISDGAGKVA FEPPARIGQKVFAVNFYDWFV	28.6	24.1	22.7	1.1	1.1	0.9
A6L-4-H5-IR		YRGMLVLGRIQDGAGKVA SEPPARIGQKVFAVNFYDWFV	37.2	24.6	23.1	1.1	1.1	0.9
A6L-4-H3-IR		QRGMLVLGGVSDGAGKVA SDPPASIGQNVFAVNFYDWFV	37.1	9.1	7.2	1.3	1.3	0.8
A6L-4-E5-IR		YFGMLILDRI SDGASKV SEPPASIGQKVFAVNFYDWFV	42.1	30.6	24.4	1.3	1.3	0.8
A6L-3-C5-IR		YRGMLVLDRI SDGAGKVA SEQPARIGQEVFAVNFYDWFV	42.2	21.9	17.5	1.2	1.2	0.8
A6L-4-G6-IR		YRGMLDLGRISGGVGKVA SEPARIGQKVFAVNFYDWFV	29.8	4.3	2.8	1.5	1.5	0.7
A6L-3-D4-IR		QRGMMVLGRISDGAGEVA SEKVFAVNFYDWFV	39.9	12.4	8.4	1.5	1.5	0.7
A6L-3-A7-IR		QRGMLVLGRVSDGAGKVA SDAPPARIGQKVFAVNFYDWFV	31.0	21.2	14.0	1.5	1.5	0.7
A6L-3-A6-IR		QRGMLVLGRMSDGAGKVA FEPPARIGQGVFAVNFYDWFV	25.5	12.3	8.8	1.4	1.4	0.7
A6L-4-E7-IR		QRGTLVLGRISDGAGKAA SEPPARIGQNVFAVNFYDWFV	38.4	12.5	7.1	1.7	1.7	0.6
A6L-3-C6-IR		QRGMLVLDRI SDGAGKVA AEPPARIGQKVFAVNFYDWFV	28.8	10.9	6.7	1.6	1.6	0.6
A6L-4-F5-IR		QRGMLVLGRISDGAGEVA SEPPARIGEKVFAVNFYDWFV	33.8	6.3	4.1	1.5	1.5	0.6
A6L-3-B7-IR		QRGILVRGRISDGAGKVG SEPPARSGEKVFAVNFYDWFV	27.6	9.4	5.0	1.9	1.9	0.5
A6L-4-F4-IR		QLGMVVLGRISDGSAGKAA SEPAARISQKVFAVNFYDWFV	38.9	17.6	9.4	1.9	1.9	0.5
A6L-4-E3-IR		QRGMLVLGRISDGDGKVA SEPPARIGQKVFAVNFYDWFV	38.0	6.9	3.8	1.8	1.8	0.5
A6L-0-E6-IR		YRGMLVLGRSSDGAGKVA FERPARIGQTVFAVNFYDWFV	31.0	31.0	1.8	17.0	17.0	0.1
A6L-0-E4-IR		YRGMLVLGRISDGAG#VASEPPARIGRKVFAVNFYDWFV	26.0	16.0	1.3	13.0	13.0	0.1
A6L-0-H3-IR		YRGMLVLGRISGGAGKAA SERPARIGQKVSAVNFYDWFV	27.0	26.0	2.0	13.0	13.0	0.1

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FIG. 1G-2

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGF ₃ R	IR	IGF ₃ R/IR	IR/IGFR
A6L-4-F8-IGFR		YRGMLVLGRISDGAGKVASVSPVRIQKQVFAVNFYDWFV	19	4	--	--	--
A6L-2-G9-IGFR		YRGMLVGRISDVAGKACDPSARIGQKVLNVNFYDWFV	26	28	--	--	--
A6L-4-E7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	39	22	--	--	--
A6L-4-G10-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	23	22	--	--	--
A6L-2-E9-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	19	22	--	--	--
A6L-2-D6-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	38	21	--	--	--
A6L-3-H12-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	34	21	--	--	--
A6L-4-A7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	24	21	--	--	--
A6L-4-B8-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	20	20	--	--	--
A6L-4-G7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	20	19	--	--	--
A6L-2-D9-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	19	19	--	--	--
A6L-4-F7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	38	18	--	--	--
A6L-4-E12-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	18	18	--	--	--
A6L-4-H7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	15	13	--	--	--
A6L-4-H12-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	14	13	--	--	--
A6L-2-A4-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	13	12	--	--	--
A6L-3-D10-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	17	4	--	--	--
A6L-2-F6-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	16	4	--	--	--
A6L-2-B11-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	15	4	--	--	--
A6L-1-B7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	26	3	--	--	--
A6L-1-D8-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	23	3	--	--	--
A6L-0-A11-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	23	3	--	--	--
A6L-3-B7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	19	3	--	--	--
A6L-1-G7-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	9	3	--	--	--
A6L-1-B9-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	20	2	--	--	--
A6L-1-C9-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	18	2	--	--	--
A6L-0-G10-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	18	2	--	--	--
A6L-1-G8-IGFR		YRGMLVGRISDVAGKVASVSPVRIQKQVFAVNFYDWFV	15	2	--	--	--

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FIG. 1H

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	--
E4D α -1-B8-IR	GFREGNFYDWFVAQVT	40.7	1.0	12.3	0.1	12.3	12.3
E4D α -3-E5-IR	GFREGQRWYWFVAQVT	39.6	2.0	1.5	1.3	0.8	0.8
E4D α -1-A1-IR	GFREGYFYDWFVAQVT	48.7	44.9	31.4	1.4	0.7	0.7
E4D α -2-D9-IR	GFREGQFYWFVAQVT	22.9	3.3	2.4	1.4	0.7	0.7
E4D α -1-B3-IR	GFREGTFYDWFVAQVT	41.8	38.6	26.5	1.5	0.7	0.7
E4D α -1-A6-IR	GFREGNFYDWFVAQVT	56.3	51.2	32.6	1.6	0.6	0.6
E4D α -1-A10-IR	GFREGAFYDWFVAQVT	48.9	42.2	26.5	1.6	0.6	0.6
E4D α -1-A8-IR	GFREGAFYDWFVAQVT	46.9	41.5	26.2	1.6	0.6	0.6
E4D α -1-B1-IR	GFREGKFYDWFVAQVT	44.1	31.1	19.7	1.6	0.6	0.6
E4D α -2-C9-IR	GFREGDFYDWFVAQVT	34.0	8.1	4.8	1.7	0.6	0.6
E4D α -1-A3-IR	GFREGTFYDWFVAQVT	45.3	40.3	22.5	1.8	0.6	0.6
E4D α -1-A9-IR	GFREGNFYDWFVAQVT	46.9	41.0	22.5	1.8	0.5	0.5
E4D α -3-F3-IR	GFREGQFYDWFVAQVT	37.2	14.1	8.0	1.8	0.6	0.6
E4D α -2-D3-IR	GFREGQFYDWFVAQVT	35.1	16.3	8.7	1.9	0.5	0.5
E4D α -2-D6-IR	GFREGQFYDWFVAQVT	33.2	5.6	2.8	2.0	0.5	0.5
E4D α -3-F10-IR	GFREGQFYDWFVAQVT	27.8	4.5	2.3	2.0	0.5	0.5
E4D α -2-D5-IR	GFREGYFYDWFVAQVT	43.8	23.8	11.4	2.1	0.5	0.5
E4D α -3-F4-IR	GFREGDFYDWFVAQVT	25.9	7.6	3.7	2.1	0.5	0.5
E4D α -3-E3-IR	GFREGSFYDWFVAQVT	34.6	4.0	1.9	2.1	0.5	0.5
E4D α -3-F8-IR	GFREGSFYDWFVAQVT	20.9	16.0	7.4	2.2	0.5	0.5
E4D α -2-C1-IR	GFREGQFYDWFVAQVT	43.1	11.6	5.0	2.3	0.4	0.4
E4D α -1-B4-IR	GFREGIFYDWFVAQVT	45.3	6.6	2.9	2.3	0.4	0.4

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FIG. 11-1

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR	
	<u>GFREGNFYDWFVAQVT</u>	--	--	--	--	--	
E4D α -4-H5-IR	GFREGSFYEFQAQVT	47.2	36.0	14.7	2.4	0.4	
E4D α -1-B12-IR	GFREGNFYDWFQAQVT	47.6	33.4	13.8	2.4	0.4	
E4D α -4-G2-IR	GFREGSFYDWFVAQVT	23.4	20.4	8.6	2.4	0.4	
E4D α -3-F9-IR	GFREGDFYDWFVAQVT	36.2	15.6	6.3	2.5	0.4	
E4D α -4-G6-IR	GFREGDFYQWFVAQVT	26.0	4.9	2.0	2.5	0.4	
E4D α -4-H9-IR	GFREGGFYDWFVAQVT	47.8	24.8	9.5	2.6	0.4	
E4D α -2-C10-IR	GFREGDFYGFQAQVT	42.4	23.2	9.0	2.6	0.4	
E4D α -1-B2-IR	GFREGVFYDWFVAQVT	39.4	18.7	7.2	2.6	0.4	
E4D α -3-F12-IR	GFREGGFYEFQAQVT	38.9	16.6	5.6	3.0	0.3	
E4D α -2-D11-IR	GFREGSFYDWFQAQVT	40.2	11.1	3.3	3.4	0.3	
E4D α -4-H2-IR	GFREGNFYEFQAQVT	37.8	33.9	8.2	4.1	0.2	
E4D β -4-A12-IR	GFREGKFYDWFQAQVT	41.1	8.3	28.7	0.3	3.5	14/122
E4D β -4-A10-IR	GFREGGFYEFVAQVT	5.8	1.2	2.4	0.5	2.0	
E4D β -4-E10-IR	GFREGRFYDWFVAQVT	9.6	1.2	2.2	0.5	1.8	
E4D β -4-B11-IR	GFREGTFYDWFVAQVT	36.1	15.2	26.9	0.6	1.8	
E4D β -4-C10-IR	GFREGGFYEFQAQVT	27.8	13.3	23.7	0.6	1.8	
E4D β -4-E8-IR	GFREGDFYEFQAQVT	28.7	16.7	28.2	0.6	1.7	
E4D β -4-G7-IR	GFREGHFYDWFQAQVT	30.9	14.7	24.7	0.6	1.7	
E4D β -4-C8-IR	GFREGGFYDWFVAQVT	35.5	22.5	32.9	0.7	1.5	
E4D β -4-A8-IR	GFREGSFYDWFVAQVT	31.2	14.5	22.2	0.7	1.5	
E4D β -4-A9-IR	GFREGSFYDWFQAQVT	35.8	9.0	13.1	0.7	1.5	
E4D β -4-G11-IR	GFREGTFYDWFQAQVT	28.9	9.7	13.6	0.7	1.4	
E4D β -4-B9-IR	GFREGNFYEFQAQVT	27.2	9.1	12.5	0.7	1.4	
E4D β -4-F10-IR	GFREGSFYNWFQAQVT	7.7	1.5	2.1	0.7	1.4	
E4D β -4-D12-IR	GFREGNFYDWFVAQVT	41.1	27.2	36.1	0.8	1.3	
E4D β -4-B8-IR	GFREGDFYDWFVAQVT	35.9	27.0	35.2	0.8	1.3	
E4D β -4-G10-IR	GFREGAFYDWFQAQVT	38.5	25.5	33.7	0.8	1.3	
E4D β -4-D9-IR	GFREGSFYDWFQAQVT	34.1	19.3	25.7	0.8	1.3	

FIG. 11-2

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	
	<u>GFREGNFYDWFFAAQVT</u>	--	--	--	--	--	
E4Dβ-4-F8-IR	GFREGSFYDWFFAAQVT	39.3	35.6	44.4	0.8	1.2	
E4Dβ-4-E12-IR	GFREGSFYEWFDAQVT	40.2	27.8	33.4	0.8	1.2	
E4Dβ-4-H12-IR	GFREGAFYDWFEAQVT	41.2	27.1	32.3	0.8	1.2	
E4Dβ-4-C9-IR	GFREGQFYDWFFAAQVT	38.0	22.5	27.6	0.8	1.2	15/122
E4D□-4-H9-IR	GFREGNFYDWFFAAQVT	38.7	33.3	36.6	0.9	1.1	
E4D□-4-G9-IR	GFREGDFYDWFFAAQVT	10.9	4.9	5.6	0.9	1.1	
E4Dβ-4-F12-IR	GFREGSFYEWFEAQVT	14.8	5.9	6.1	1.0	1.0	
E4Dβ-4-F9-IR	GFREGGFYDWFLAQVT	39.3	31.3	28.3	1.1	0.9	
E4Dβ-4-F7-IR	GFREGGFYAWFFAAQVT	31.0	22.2	19.5	1.1	0.9	
E4Dβ-4-B7-IR	GFREGGFYEWFF?AQVT	--	--	--	--	--	

FIG. 1I-3

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
E4D-2-E7-IGFR	GFREGNFYDWFVAQVT	--	--	--	--	--
E4D-2-C11-IGFR	GFREGDFYDWFRAQVT	20.8	22.8	--	--	--
E4D-2-B1-IGFR	GFREGSFYDWFVAQVT	21.5	22.6	--	--	--
E4D-2-D10-IGFR	GFREGDFYDWFQAQVT	22.0	22.5	--	--	--
E4D-2-A9-IGFR	GFREGGFYDWFQAQVT	20.6	22.1	--	--	--
E4D-2-E5-IGFR	GFREGDFYDWFVAQVT	17.4	21.5	--	--	--
E4D-2-H9-IGFR	GFREGDFYDWFQAQVT	24.2	21.2	--	--	--
E4D-1B-C4-IGFR	GFREGGFYDWFVAQVT	19.1	20.7	--	--	--
E4D-2-E10-IGFR	GFREGDFYDWFQAQVT	24.3	20.5	--	--	--
E4D-2-F4-IGFR	GFREGNFYDWFQAQVT	21.0	20.5	--	--	--
E4D-2-C10-IGFR	GFREGNFYDWFQAQVT	25.0	20.2	--	--	--
E4D-3-D8-IGFR	GFREGNFYDWFQAQVT	22.8	20.1	--	--	--
E4D-3-F9-IGFR	GFREGQFYDWFQAQVT	21.1	19.8	--	--	--
E4D-1B-E5-IGFR	GFREGSFYDWFQAQVT	22.6	19.7	--	--	--
E4D-2-F3-IGFR	GFREGDFYDWFQAQVT	24.2	18.8	--	--	--
E4D-3-D5-IGFR	GFREGHFYDWFVAQVT	23.6	18.0	--	--	--
E4D-3-G10-IGFR	GFREGQFYDWFQAQVT	22.2	18.0	--	--	--
E4D-2-F6-IGFR	GFREGQFYDWFQAQVT	22.1	17.6	--	--	--
E4D-2-F7-IGFR	GFREGQFYDWFQAQVT	24.6	17.5	--	--	--
E4D-3-B7-IGFR	GFREGDFYDWFQAQVT	19.0	17.5	--	--	--
E4D-1B-C12-IGFR	GFREGNFYDWFVAQVT	23.0	16.4	--	--	--
E4D-3-B1-IGFR	GFREGSFYDWFQAQVT	23.0	16.1	--	--	--
E4D-2-E2-IGFR	GFREGHFYDWFQAQVT	21.6	16.0	--	--	--
E4D-2-D1-IGFR	GFREGDFYDWFQAQVT	21.9	14.1	--	--	--
E4D-1-D4-IGFR	GFREGHFYDWFQAQVT	24.5	13.2	--	--	--
E4D-1B-A10-IGFR	GFREGYFYDWFQAQVT	18.9	12.4	--	--	--
E4D-1B-A3-IGFR	GFREGHFYDWFQAQVT	23.9	10.8	--	--	--
E4D-1-B5-IGFR	GFREGDFYDWFQAQVT	22.2	10.8	--	--	--
	GFREGTFYDWFQAQVT	19.0	10.8	--	--	--

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FIG. 1J-1

Clone Design	Sequence	Ratios over Background		Comparisons	
	<u>GFREGNFYDWFVAQVT</u>	E-Tag	IGF ₃ R	IGFR/IR	IR/IGFR
E4D-1B-B8-IGFR	GFREGDYGGWFEAQVT	23.8	10.7	--	--
E4D-1-G7-IGFR	GFREGDFYAWFMAQVT	14.3	10.5	--	--
E4D-1B-A11-IGFR	GFREGNFYEWFLAQVT	24.0	10.0	--	--
E4D-1-C3-IGFR	GFREGSFYDWFDAQVT	15.8	9.3	--	17/122
E4D-2-H1-IGFR	GFREGNFYDQFVAQVT	19.6	4.9	--	--
E4D-1-C2-IGFR	GFREGHFYEWFAAQVT	11.5	4.5	--	--
E4D-1B-A12-IGFR	GFREGNFYEWFVAQVT	18.4	3.5	--	--
E4D-1B-A1-IGFR	GFREGKFYDWFVAQVT	22.5	2.9	--	--
E4D-2-A3-IGFR	GFREGMFDVQLLAQVT	22.7	2.1	--	--

FIG. 1J-2

Clone Design Parental	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
	XXXXXXFHENFYDWFVRQVSXXXXXX VTFTSAVFHENFYDWFVRQVS	--	--	--	--	--
H2CA-4-F11-IR	TYKARFLHENFYDWFNRQVSQYFGRV	29.8	17.5	16.3	1.1	0.9
H2CA-4-E10-IR	QRLSLHEQFYDWFVGQVSPLGAGG	37.7	2.2	18.1	0.1	8.2
H2CA-4-G3-IR	GGKVNFDHEDFYDWFVQFSGVGSDD	31.2	4.4	18.8	0.2	4.3
H2CA-3-A11-IR	LVGDAPFHEDFYDWFARQVFGCCQEQ	36.1	13.4	25.7	0.5	1.9
H2CA-4-F8-IR	TGAEVSFHENFYDWFDRQYSSWLDNRD	35.6	12.1	22.0	0.5	1.8
H2CA-4-G4-IR	QPHSSRLHESFYDWFDRQVPWYALDR	36.0	21.1	33.5	0.6	1.6
H2CA-4-F4-IR	SRALAAVHEQFYDWFVRQVSGLDWGY	37.1	23.3	34.3	0.7	1.5
H2CA-4-H10-IR	QPKDGTLHENFYDWFVRQVSSSGWVG	39.8	25.0	35.6	0.7	1.4
H2CA-4-F1-IR	RGRLIQLHEDFYDWFRLRQVSGMGGS	33.5	5.1	6.6	0.8	1.3
H2CA-3-D5-IR	QRGAPKSDENFYDWFVRQVLRFGEND	36.1	19.6	25.1	0.8	1.3
H2CA-4-E11-IR	AARTSLFHEDFYDWFDRQVRQEGMWG	39.3	24.3	31.9	0.8	1.3
H2CA-3-B6-IR	GTSNHSLHENFYDWFVRQLSSVQSSG	8.2	2.6	3.2	0.8	1.2
H2CA-3-A9-IR	VSHVHLFHENFYDWFVRQLAAEGFSG	35.9	9.9	12.1	0.8	1.2
H2CA-4-H5-IR	GRQDSGLHEFYDWFVRQVQGEVALG	37.3	30.1	36.2	0.8	1.2
H2CA-3-C9-IR	SNDERQFHETFYDWFVRQVSADGADR	38.6	35.4	37.3	1.0	1.1
H2CA-3-A10-IR	LSTEQRFEKIFYDWFVHQVSTSGGGT	29.3	5.1	5.6	0.9	1.1
H2CA-3-A3-IR	SLSRQFHENFYDWFARQVSELEGVV	37.2	16.9	19.1	0.9	1.1
H2CA-4-G8-IR	IPGRRSLHENFYDWFVRQVSPGGSA	29.2	28.6	32.2	0.9	1.1
H2CA-4-G9-IR	TQKAQSLDEKIFYDWFVRQVSGGLTG	32.4	29.1	31.6	0.9	1.1
H2CA-4-G10-IR	VSQLSDFHENFYDWFARQIAGQAEWT	36.1	34.4	36.4	0.9	1.1
H2CA-4-H7-IR	NGTSQALHQNFYDWFARQISGSEPGP	34.2	35.5	37.7	0.9	1.1
H2CA-4-F9-IR	VGQSVTFHGDFYDWFDRQLSGSQEFG	37.0	36.0	40.0	0.9	1.1
H2CA-4-F7-IR	TIDHPLHEQFYDWFARQVSDLESIG	37.5	36.7	39.5	0.9	1.1
H2CA-3-D10-IR	PNVGYAFHENFYDWFIRQVSIIEKAG	37.7	37.6	39.9	0.9	1.1
H2CA-3-B1-IR	SRGSGVFHESFYDWFDRQVSEWIQFG	18.7	3.6	3.5	1.0	1.0
H2CA-3-A5-IR	QPVSGSVHERFYDWFVRQVSGSAGGG	26.5	21.4	21.5	1.0	1.0
H2CA-4-F10-IR	ASQLPPVYENFYDWFDRQVSLDAQRE	32.9	22.9	22.4	1.0	1.0
		26.6	27.7	28.5	1.0	1.0

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FIG. 1K-1

		Ratios over Background				Comparisons	
		E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR	
Sequence		--	--	--	--	--	--
Clone	Design	36.6	30.6	30.9	1.0	1.0	1.0
H2CA-3-D9-IR	VSGRGAFHENFYDWFVRQVSRDEQDT	38.3	30.7	31.0	1.0	1.0	1.0
H2CA-3-C2-IR	ARPPPTVHENFYDWFVRQVSETWRQD	34.1	30.7	30.4	1.0	1.0	1.0
H2CA-4-G1-IR	QGGDRLFERFYDWFDRLVSSDSTGE	33.9	31.0	31.8	1.0	1.0	1.0
H2CA-4-E2-IR	QHIAAGLHENFYDWFIRQVSGVNPFA	38.9	31.1	31.4	1.0	1.0	1.0
H2CA-4-H9-IR	QPNDDLHENFYDWFVRQVSNVADGG	33.0	31.1	29.8	1.0	1.0	1.0
H2CA-3-D2-IR	PVEFTVYHDNFYDWFARQVSDGLGQF	35.3	31.4	30.0	1.0	1.0	1.0
H2CA-3-B3-IR	FCVQASIHENFYDWFVRQVAENQVFS	37.9	31.9	31.0	1.0	1.0	1.0
H2CA-4-G11-IR	GRPRGSFHENFYDWFARQVSGDGAGT	38.1	32.0	31.9	1.0	1.0	1.0
H2CA-4-F2-IR	IVGASLCHESFYDWFACQVTNLQSQG	36.9	32.3	31.6	1.0	1.0	1.0
H2CA-3-C5-IR	IGLRQMFHENFYDWFAREVSKEAGDG	36.6	32.7	32.5	1.0	1.0	1.0
H2CA-3-B2-IR	LGAIEGHGNFYDWFVRQVSLDVGGE	35.5	32.8	33.3	1.0	1.0	1.0
H2CA-3-B11-IR	LNALQQLHENFYDWFGRQVSATPPGG	35.9	33.0	33.4	1.0	1.0	1.0
H2CA-4-G2-IR	VGNCDTFPENFYDWFACQVSELGGMN	33.3	33.0	32.9	1.0	1.0	1.0
H2CA-3-A4-IR	FSQDGNFHENFYDWFDRQVSLVGAGT	39.5	33.7	33.7	1.0	1.0	1.0
H2CA-4-H3-IR	PAGNRALHESFYDWFVRQVSEFQLGA	35.3	34.0	35.6	1.0	1.0	1.0
H2CA-4-G5-IR	DRLRARFNENFYDWFDRQVSGQSMF	35.7	34.7	34.9	1.0	1.0	1.0
H2CA-4-E8-IR	VLGVAQFHDKFYDWFARQVSQLESAG	36.2	35.0	33.5	1.0	1.0	1.0
H2CA-4-G6-IR	GVVGAFHEQFYDWFDRQVSAAFKGD	37.6	36.5	35.3	1.0	1.0	1.0
H2CA-3-B7-IR	DESEMRLHEQFYDWFARLVSLGGSA	39.8	36.5	35.1	1.0	1.0	1.0
H2CA-3-B4-IR	EGGGVAIHENFYDWFDRQVSLQWSD	40.2	36.7	35.9	1.0	1.0	1.0
H2CA-3-C7-IR	SRIVSRFHENFYDWFVRQVSGDAPVQ	37.3	37.0	36.3	1.0	1.0	1.0
H2CA-4-E5-IR	IPAGAQLHENFYDWFARQVSGEDGGA	39.7	37.6	37.6	1.0	1.0	1.0
H2CA-4-E7-IR	GSSAAGFDEQFYDWFDRQVSEAFRDG	39.4	37.7	37.6	1.0	1.0	1.0
H2CA-3-B9-IR	RLALRTFHQDFYDWFVRQVAEDTDP	38.8	38.0	37.8	1.0	1.0	1.0
H2CA-4-F5-IR	QGSFAVLHENFYDWFARQVSGVEGLA	41.9	38.9	38.0	1.0	1.0	1.0
H2CA-3-B10-IR	QGNMSALHENFYDWFVRQVSEADRVD	37.8	7.3	6.3	1.2	0.9	0.9
H2CA-3-A12-IR	VAYPALLHEQFYDWFVRQVSAVAGTT	36.8	22.5	19.2	1.2	0.9	0.9
H2CA-3-A8-IR	PDTINSQHKNFYDWFVRQVSGVGTSS						

FIG. 1K-2

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
H2CA-3-D12-IR	XXXXXXXXFHENFYDFWFRQVSGXXXXXX	--	--	--	--
H2CA-3-B5-IR	SEDVDSRHENFYDFWFRQVSGIGLQD	36.8	34.1	1.2	0.9
H2CA-4-E1-IR	PAPADAFDHNFYDFWFRQLSATTIQ	38.8	35.2	1.2	0.9
H2CA-3-D3-IR	MVQRISIHENFYDFWFRQISGSAVPP	29.8	12.5	1.1	0.9
H2CA-4-E3-IR	GNVRGQFHGQFYDFWFRQVSGSEGDA	33.1	29.9	1.1	0.9
H2CA-4-E12-IR	PDAEKQFHETFYGFWFRQISEDSANS	33.3	32.3	1.1	0.9
H2CA-3-A6-IR	FGRGVHCDENFYDFWFRQVSGALLEG	36.0	32.4	1.1	0.9
H2CA-4-E9-IR	ETPLTELHEQFYDFWFRQVSGFPGV	34.0	33.1	1.1	0.9
H2CA-4-F3-IR	QHRGPHFHEFYDFWFRQVSSAVPSD	38.8	33.7	1.1	0.9
H2CA-4-H6-IR	RQDPGLFHDNFYDFWFRQVSAWDGQE	41.0	34.2	1.1	0.9
H2CA-4-H2-IR	QAAVGVCNKDFYAWFACQVREDFAKA	37.1	34.5	1.1	0.9
H2CA-3-D1-IR	RNNNLQFNENFYDFWFRQVSRALRGGG	41.8	35.3	1.1	0.9
H2CA-3-C1-IR	RSEQYRFHENFYDFWFRQVSRMGLLG	38.7	35.5	1.1	0.9
H2CA-3-D8-IR	GAGGRDFEDFYDFWFRQVSGQVTS	34.5	35.5	1.1	0.9
H2CA-4-H4-IR	SPEGNLVHDQFYDFWFRQVSSSTAGT	39.9	36.1	1.1	0.9
H2CA-4-F6-IR	QGGLGDFEDFYDFWFRQVSRDRAD	37.8	36.7	1.1	0.9
H2CA-4-E4-IR	LSQGVGFQENFYDFWFRQVSGWDGRD	38.5	37.0	1.1	0.9
H2CA-3-C11-IR	VFERSRCHDNFYDFWFRQVSGQADGG	38.7	37.5	1.1	0.9
H2CA-3-C4-IR	LLASRAFHENFYDFWFRQVSGTQPPG	38.6	38.0	1.1	0.9
H2CA-4-E6-IR	VPDAQIFHESFYDFWFRQASAGGPAD	40.3	38.3	1.1	0.9
H2CA-3-D7-IR	ANQMGRFHDNFYDFWFRQVSRYERGT	41.9	38.4	1.1	0.9
H2CA-3-A7-IR	PSRKDGLHQSFYDFWFRQVDMEGRA	39.3	38.8	1.1	0.9
H2CA-4-G12-IR	QAVTRRFHENFYDFWFRQVSEEGGS	42.5	39.2	1.1	0.9
H2CA-3-D6-IR	GYAVGQYQANFYDFWFRQVSGMSNGG	35.3	15.2	1.3	0.8
H2CA-4-H12-IR	GHQRDLHESFYDFWFRQVSEAEAGG	37.6	19.4	1.3	0.8
H2CA-3-D11-IR	DRPSSFIHENFYDFWFRQVSGSSG	39.4	36.2	1.3	0.8
H2CA-3-C12-IR	ERTAEHLHEQFYDFWFRQVSAWDGES	40.0	38.4	1.3	0.8
	LTSQLLHSHEDFYDFWFRQVSGVGGSG	38.1	32.9	1.2	0.8
	PDRSDRLDDNFYDFWFRQVSGVINED	38.5	38.4	1.2	0.8

FIG. 1K-3

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGF β R	IR	IGFR/IR	IR/IGFR	
H2CA-4-G7-IR	XXXXXXXXFHENFYDWFVRQVSXXXXXX	--	--	--	--	--	21/122
H2CA-3-C6-IR	RAGGVGLHDNFYDWFVRQVSGGDSGP	35.9	34.7	23.7	1.5	0.7	
H2CA-3-B8-IR	ADCVQLHENFYDWFRRQVCNLQEGM	38.7	37.6	28.2	1.3	0.7	
	RQGHAGFHDNFYDWFVRQVSGSTPQV	37.8	19.6	9.9	2.0	0.5	

FIG. 1K-4

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Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXFHENFYDFWFRQVSXXXXXX	--	--	--	--	--
	VTFTSAVFHENFYDFWFRQVS	29.8	17.5	16.3	1.1	0.9
H2CA-4-G9-IGFR	GIISQSCPESFYDFWFRQVSDPWWCW	8.6	9.5	0.6	16.0	0.1
H2CA-4-H6-IGFR	VGRASGFPENFYDFWFRQLSLQSGEQ	4.9	10.5	0.7	14.6	0.1
H2CA-4-F-IGFR5	VGYQGQGDENFYDFWFRQVSGRLGVQ	5.5	9.7	0.8	12.3	0.1
H2CA-4-H8-IGFR	SACQFDCHENFYDFWFRQVSGGAAYG	5.6	9.2	1.0	9.4	0.1
H2CA-4-F11-IGFR	SAAQLFFQESFYDFWFRQVAESSQPN	3.5	6.8	1.0	6.7	0.1
H2CA-4-F6-IGFR	AVRATRFDEAFYDFWFRQISDQGQNK	3.9	7.3	1.1	6.4	0.2
H2CA-4-F10-IGFR	VNQSGSIHENFYDFWFRQVSHQRGVR	4.9	5.7	1.0	5.9	0.2
H2CA-1-A3-IGFR	APDPSDFQEIFYDFWFRQVSRMPGGG	7.7	3.8	0.8	5.1	0.2
H2CA-3-C8-IGFR	SSCDGAGHESFYEWFRQVSGCRSV	15.1	5.6	1.2	4.8	0.2
H2CA-2-B9-IGFR	RAGSSDFHEDFYEWFRQVSLSLK GK	9.3	7.0	1.7	4.2	0.2
H2CA-4-H4-IGFR	QAVQPGFHEEFYDFWFRQVSTGVGGG	3.9	4.1	1.0	4.2	0.2
H2CA-4-F7-IGFR	SSIIGGFHENFYDFWFSRQLSQSPPLK	1.5	3.2	0.8	4.1	0.2
H2CA-3-D6-IGFR	QSPVGSSEHEDFYDFFFRQVAQSAHQ	8.3	9.0	2.2	4.0	0.3
H2CA-3-D8-IGFR	NYRRQVFNGNFYDFWFRQVFSLVTPG	10.9	7.2	1.8	4.0	0.3
H2CA-4-G11-IGFR	TLDGGSFEEQFYDFWFRQLSYRTNPD	10.8	9.5	2.5	3.9	0.3
H2CA-4-F1-IGFR	FYVQQWGHENFYDFWFRQVSGGGAG	5.8	3.5	0.9	3.8	0.3
H2CA-3-D7-IGFR	LRRQAPVEENFYDFWFRQVSGDRVGG	13.3	3.0	0.8	3.7	0.3
H2CA-1-A7-IGFR	RCGRELYHSTFYDFWFRQVAGRTCPS	8.0	2.2	0.6	3.7	0.3
H2CA-2-B4-IGFR	CCLLCRFQNFYDFWFRVCQGISRLRPL	3.5	4.1	1.1	3.6	0.3
H2CA-2-B3-IGFR	PPLASDLDVQFYGWFRQVSPPPGRGG	7.7	3.8	1.0	3.6	0.3
H2CA-2-B2-IGFR	GAPVDQLHEDFYDFWFRQVSAATG	4.1	3.4	1.0	3.5	0.3
H2CA-3-D4-IGFR	RSASGSLPEQFYDFWFRQVSLSGTDK	17.6	13.8	4.1	3.4	0.3
H2CA-4-F2-IGFR	SRVTVFHENFYDFWFRQLSDSAISG	9.3	12.8	4.2	3.0	0.3
H2CA-3-D11-IGFR	DERGGKFREDFYDFWFRQVSESFRFGQ	12.2	6.9	2.3	3.0	0.3
H2CA-4-H9-IGFR	RGAVAGFHDQFYDFWFRQVSRVHKFG	8.7	5.6	1.9	3.0	0.3
H2CA-2-B11-IGFR	AICDAGFHEHFYDFWFRQVSDCGRQS	11.9	4.6	1.6	3.0	0.3
H2CA-3-E8-IGFR	LGYQEPFQNFYDFWFRQVSGAENAG	13.2	6.3	2.2	2.9	0.3

FIG. 1L-1

[illegible]

FIG. 1M-1

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	--
H2CB α -3-D11-IR	XXXXXXFHXXFYXWFXXXXXX	27.8	13.0	24.8	0.5	1.9	1.9
H2CB α -3-H12-IR	GPRGQRLHDAFYSWFDALRVN	27.4	7.2	12.4	0.6	1.7	1.7
H2CB α -3-A10-IR	LGTIAVFHELFGWFERQLGG	27.1	13.2	22.3	0.6	1.7	1.7
H2CB α -3-A5-IR	LGGYCGENCQFYRWFDNLADR	28.3	16.1	28.1	0.6	1.7	1.7
H2CB α -3-C4-IR	FSGWADYQSGFYQWFAEELAN	30.7	17.2	29.2	0.6	1.7	1.7
H2CB α -3-B8-IR	WGPFSVFDESFYRWFAQASDD	25.6	11.3	18.6	0.6	1.6	1.6
H2CB α -3-H11-IR	PRNEGLVHGLFYDWFQALSG	28.8	14.0	22.4	0.6	1.6	1.6
H2CB α -3-E10-IR	DEGGAPLDVMFYRWFEQAVRG	27.7	14.3	23.0	0.6	1.6	1.6
H2CB α -3-C2-IR	QSGNRGSHGAFYSWFRDVLAN	28.4	17.0	26.7	0.6	1.6	1.6
H2CB α -3-F6-IR	MRQRDGFNSSFYGWFAAALGE	27.3	14.5	21.8	0.7	1.5	1.5
H2CB α -3-D4-IR	SEERKKVHSQFYSWFDRQLLG	29.0	18.9	27.1	0.7	1.4	1.4
H2CB α -3-A7-IR	PSPNAPFHGGFYDWFEDWVQGS	29.1	19.4	26.9	0.7	1.4	1.4
H2CB α -3-H4-IR	FHRPGSFNTNFYQWFEDDQMNQ	27.2	20.1	27.9	0.7	1.4	1.4
H2CB α -3-B7-IR	SDDSTLNGRFYTWFEHMQLLD	28.6	18.0	23.6	0.8	1.3	1.3
H2CB α -3-F9-IR	QGGGFHEGFYSWFRSQSLL	26.1	19.1	24.3	0.8	1.3	1.3
H2CB α -3-H6-IR	SGSRPVFHEQFYEWFEVDQLGL	24.8	21.6	27.3	0.8	1.3	1.3
H2CB α -3-F5-IR	GGSSQAFHGAFYEWFSQAQLRG	29.4	22.0	27.8	0.8	1.3	1.3
H2CB α -3-A2-IR	AFVSERVNQRFYDWFDRDQMR	30.7	22.5	29.1	0.8	1.3	1.3
H2CB α -3-F3-IR	VRHPTRFHDEFYRWFTTEQLTT	16.3	6.7	9.0	0.7	1.3	1.3
H2CB α -3-G6-IR	ARLLNIFDRGFYNWFQRQLDE	24.9	21.0	24.4	0.9	1.2	1.2
H2CB α -3-G7-IR	PSLSSNLHESFYRWFDQLVST	24.4	18.7	23.0	0.8	1.2	1.2
H2CB α -3-C5-IR	FAFGLGFHQGFYDWFHQAQLEG	26.4	21.2	25.4	0.8	1.2	1.2
H2CB α -3-G1-IR	VSATVMLHREFYDWFGLQLLD	26.9	21.5	26.3	0.8	1.2	1.2
H2CB α -3-E3-IR	GGVSGVLHDRFYSWFERQLAG	24.2	17.2	19.3	0.9	1.1	1.1
	GLGIASFHEGFYSWFTTAQLGA						

FIG. 1M-2

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF ₃ R	IR	IGFR/IR IR/IGFR
	XXXXXXXXXXXXXX	--	--	--	--
H2CBa-3-A9-IR	RVDAALNAGFYEWFRGVIQG	30.5	21.7	24.1	0.9 1.1
H2CBa-3-C11-IR	GGAGRSFHDAFYEWFERQMAG	26.4	21.8	23.2	0.9 1.1
H2CBa-3-B4-IR	EGARQGFHARFYSWFAQQAL	30.9	22.0	24.3	0.9 1.1
H2CBa-3-F11-IR	VLLPGVVHGGFYDWFSRQLSS	24.5	22.5	23.9	0.9 1.1
H2CBa-3-G10-IR	GALSDRYNNVFYDWFREQLLG	28.3	23.6	27.1	0.9 1.1
H2CBa-3-D7-IR	PDSFMSLHQRFYSWFQAQVGT	31.4	23.6	25.3	0.9 1.1
H2CBa-3-E2-IR	RVYKANFHNEFYGWFREQLLG	26.8	24.0	25.7	0.9 1.1
H2CBa-3-B5-IR	HSGMRDVHARFYSWFSEQLSG	28.7	25.0	26.4	0.9 1.1
H2CBa-3-C7-IR	ARLLERFQDPFYEWFEETLMGD	30.0	25.2	28.7	0.9 1.1
H2CBa-3-G9-IR	RNSSGNFHDKFYNWFEAQLKG	27.8	25.2	26.7	0.9 1.1
H2CBa-3-A12-IR	GSMSPVENDQFYGWFRLDVLDE	28.0	26.4	28.7	0.9 1.1
H2CBa-3-C9-IR	SCTGRQFDGCFYAWFEDQLVG	32.1	28.7	31.9	0.9 1.1
H2CBa-3-B10-IR	GIAVQSLHDSFYRWFDNALGS	33.5	30.8	33.2	0.9 1.1
H2CBa-3-E1-IR	IGPPGSLHRGFYDNWFAEQVEA	31.7	30.5	29.0	1.1 1.0
H2CBa-3-G12-IR	GAAGISFHRGFYDNWFAAQVRD	29.1	31.4	29.8	1.1 1.0
H2CBa-3-F7-IR	GVDVTDFHKDFYSWFQRQLNG	23.2	20.7	20.3	1.0 1.0
H2CBa-3-G8-IR	WAGRAGIHGGFYEWFNRLRG	22.8	20.9	20.4	1.0 1.0
H2CBa-3-C6-IR	LGQLAAFHILGFYEWFESEAVAA	26.7	21.2	22.0	1.0 1.0
H2CBa-3-H9-IR	VHSVSRNLNVGFYQWFQDQLSG	23.4	22.5	22.0	1.0 1.0
H2CBa-3-H8-IR	LGLMAIFDRGFYGFWEQQLSG	23.5	23.4	23.2	1.0 1.0
H2CBa-3-F2-IR	VARGSSLHDDFYEWFAFASQLRT	25.5	24.3	25.2	1.0 1.0
H2CBa-3-D5-IR	LGYIGALNTQFYSWFADLVGS	26.7	24.5	25.6	1.0 1.0
H2CBa-3-D10-IR	EDSRLRLHEGFYGWFRKQLGD	26.8	24.9	24.9	1.0 1.0
H2CBa-3-F10-IR	GRDNMKFHS GFYDWFTQQLAG	25.7	25.6	26.1	1.0 1.0

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FIG. 1M-3

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag --	IGF ₃ R --	IR --	IGF ₃ R/IR --	IR/IGF ₃ R --	--
H2CBα-3-D6-IR	AGVMGGFHQEFY L WFERALSN	27.9	26.0	25.8	1.0	1.0	1.0
H2CBα-3-H3-IR	AGHVQVYDGYGWFREQLGA	27.0	26.9	26.2	1.0	1.0	1.0
H2CBα-3-F4-IR	FVQNI G FDYDFY G WFFVREVEK	31.2	27.2	27.7	1.0	1.0	1.0
H2CBα-3-E9-IR	PVGIGGLHRAFYQWFQSQVDA	31.6	27.7	28.2	1.0	1.0	1.0
H2CBα-3-H10-IR	GSRQ E ADHQAFYDWFNLVLGV	26.9	27.9	28.8	1.0	1.0	1.0
H2CBα-3-G2-IR	AGGRKPFHDDFYGWF R DQLAE	29.1	28.1	28.8	1.0	1.0	1.0
H2CBα-3-B2-IR	DLASHGFHDAFY N WFSVQLNS	29.4	28.1	28.2	1.0	1.0	1.0
H2CBα-3-E8-IR	GSNGGGVHGQFYAWFVEALSG	31.5	28.4	29.1	1.0	1.0	1.0
H2CBα-3-E5-IR	RGRASTFHDGFGY G WFSQQLRF	33.0	28.7	28.9	1.0	1.0	1.0
H2CBα-3-E6-IR	SPARRVSHHDFY G WFAKQLES	29.6	29.0	28.1	1.0	1.0	1.0
H2CBα-3-E7-IR	SSDVGA F HSAFYDWFKAQLSG	30.4	30.2	30.2	1.0	1.0	1.0
H2CBα-3-C8-IR	PTVHRAFD D LFY G WFAKQVED	31.9	31.2	31.5	1.0	1.0	1.0
H2CBα-3-A4-IR	SSNTVGLDERFYAWFVDQLGA	32.2	31.9	32.6	1.0	1.0	1.0
H2CBα-3-D1-IR	PGAAEGFHSAFYDWF A QAVSG	32.9	32.5	31.5	1.0	1.0	1.0
H2CBα-3-B9-IR	MRSEASFHVEFY S WFEEQLRS	33.2	33.8	33.3	1.0	1.0	1.0
H2CBα-3-D8-IR	VSRYG Q QDGFYHWFSDLLKG	26.3	20.2	19.1	1.1	1.1	0.9
H2CBα-3-F1-IR	RPSSGGLHYGFYHWF R VQEM	28.8	28.0	26.4	1.1	1.1	0.9
H2CBα-3-A11-IR	SNIEEHFMQFY R WFSDALGN	20.5	21.5	17.7	1.2	1.2	0.8
H2CBα-3-A3-IR	ANDCLGLHAGFY G WFACQLGG	30.4	29.6	21.8	1.4	1.4	0.7

FIG. 1M-4

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag --	IGFsR --	IGFR/IR --	IR/IGFR --
H2CB β -3-E8-IR	XXXXXXXXXXXXXXXXXXXXX TGHRLGLDEQFYWWFRDALSG	15.9	1.9	0.2	6.1
H2CB β -4-F8-IR	VLTSNTLHQRFYSWFAAARRE	13.4	0.8	0.3	3.4
H2CB β -3-C4-IR	CVAQGGFQSSFYCWFAGLDID	21.1	1.3	0.3	3.1
H2CB β -3-D5-IR	NGQSSRFHTAFYDWFAAQLSG	14.0	3.3	0.3	3.1
H2CB β -3-E6-IR	SVPRGTVHDAFYQWFRFVALG	5.7	0.7	0.3	3.1
H2CB β -4-G12-IR	GARGSTFHDQFYEWFWVQLGD	6.8	1.8	0.3	3.1
H2CB β -4-F4-IR	PPGMNGFHTSFYSWFVDQLGD	17.9	1.9	0.3	3.0
H2CB β -4-F11-IR	AVGTLYHSGFYRWFERQLGG	15.0	1.7	0.3	2.9
H2CB β -3-E5-IR	ELQARGVHRNFYRWFEAQVSG	17.0	1.8	0.4	2.8
H2CB β -4-F2-IR	HRVARAFHEQFYDWFEKAVSG	15.9	1.3	0.4	2.6
H2CB β -4-G4-IR	GAMEPDYHRSFYQWFAAALGE	8.7	1.4	0.4	2.6
H2CB β -3-C8-IR	CPDRQSVDDRFYNWFADALAS	4.9	1.4	0.4	2.3
H2CB β -4-F10-IR	GGAQISFHERFYQWFLQEAAG	10.2	1.0	0.4	2.3
H2CB β -4-H4-IR	HKRGIVQHGAFYAWFDSLSSG	20.8	4.2	0.4	2.3
H2CB β -4-G6-IR	QASDNRSDDGYLWFEKLLSS	14.5	5.6	0.7	1.5
H2CB β -4-H1-IR	DRGRMGVDEGFYNWFARQMGE	17.0	10.1	0.8	1.3

FIG. 1M-5

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
Parental	XXXXXXXXXXFYXWFXXXXXXXX	--	--	--	--
H2CB-3-D2-IGFR	VTFTSAVFHENFYDWFRQVS	29.8	17.5	16.3	1.1
H2CB-3-C12-IGFR	TASQECFDDGFYGFRAWRCT	22.9	18.6	11.8	1.6
H2CB-3-B11-IGFR	SLDWRWSEEPFYRWFQALAG	17.3	19.6	13.0	1.5
H2CB-4-E2-IGFR	CMSLSDCHRKFYGFWSQGGG	24.6	17.1	11.9	1.4
H2CB-3-A5-IGFR	LALCRRSPGSFYGFQAAVGC	22.4	21.0	16.5	1.3
H2CB-4-G12-IGFR	PRSATMSDGGFYWFFASQLGL	28.8	26.1	22.6	1.2
H2CB-3-B2-IGFR	LRRSSVFHDPFY*ISRLVGG	23.7	23.8	19.4	1.2
H2CB-3-D1-IGFR	ARLQQQFHGGFYWFRAQVSP	23.0	19.9	16.4	1.2
H2CB-3-B6-IGFR	AQLDNLCHEPFYWFCAVTR	21.5	19.5	15.7	1.2
H2CB-4-F7-IGFR	WTCDTAFHQDFYQWFCDKLV	16.3	4.5	3.7	1.2
H2CB-4-G8-IGFR	GKEGFLDRDFYWWFREQLGP	22.0	19.0	18.0	1.1
H2CB-3-D4-IGFR	GRAPSSFDCDFYCWFRNQVS	20.2	18.6	16.5	1.1
H2CB-3-D5-IGFR	DVEAETQHRLEFYAWFLSQLGS	21.9	18.3	16.9	1.1
H2CB-4-E6-IGFR	ISVTAVFHDGFYGFNEQVSK	21.4	17.9	16.4	1.1
H2CB-3-C2-IGFR	NSEHGRLDVDFYGFARVIOQ	19.6	15.8	14.8	1.1
H2CB-3-A6-IGFR	GPLDGCQDGFYGFWMQVST	18.8	12.2	10.8	1.1
H2CB-4-H12-IGFR	KRSAYNFHDPFYDWFRMQLSG	26.8	29.0	28.1	1.0
H2CB-3-B10-IGFR	ASEPGGYLDPFYGFREQLRA	23.9	28.3	28.1	1.0
H2CB-4-F11-IGFR	NRDGGVHSGFYFNWFRQLSG	27.1	27.5	27.3	1.0
H2CB-4-G11-IGFR	ASKGSSLHNDFYGFQAQLAR	25.5	25.5	24.6	1.0
H2CB-4-E12-IGFR	ANVSMWIOVGFYDWFDAQLRQ	25.3	25.4	25.3	1.0
H2CB-4-G10-IGFR	RTSPGSLHDPFYDWFQQQLGG	27.8	24.9	24.7	1.0
H2CB-3-B9-IGFR	PGVMSSFHGGFYSWFREQLNG	25.1	24.6	24.2	1.0
H2CB-3-B7-IGFR	CLANSEHDHSFYGFWCQALGG	25.6	23.3	23.7	1.0
H2CB-4-H4-IGFR	GGSMGMHGSFYEWFAQLRLS	24.0	23.2	23.5	1.0
	RPQGGSIHAGFYQWFRDAVAG	23.5	23.1	23.8	1.0

FIG. 1N-1

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag --	IGFsR --	IR --	IGFR/IR --
H2CB-4-H10-IGFR	XXXXXXXXXXFYXWXXXXXXXXXX	21.9	22.4	23.3	1.0
H2CB-4-H5-IGFR	GALSSLFDAAFYDWFNRLQLEG	22.3	22.3	21.6	1.0
H2CB-4-G7-IGFR	KVDLRGFHDGFGYGFARQLAG	23.1	21.6	20.6	1.0
H2CB-4-F4-IGFR	CSGLQRCHDSFYSWFESVRE	21.3	20.9	21.3	1.0
H2CB-3-D8-IGFR	DSLGISFHEGFDWFRRLQDM	20.0	20.5	21.6	1.0
H2CB-4-E4-IGFR	SGVFNGTFYDWFRILQGE	21.6	20.5	21.2	1.0
H2CB-4-E5-IGFR	GYREMRSDLGFYQWFRDQLGL	22.0	19.9	20.9	1.0
H2CB-4-E8-IGFR	SVFMQHDHVGFYAWFRSLMEE	21.1	19.7	20.7	1.1
H2CB-3-D12-IGFR	FRHITEVDRSFYGFVEQLRG	26.6	17.3	16.8	1.0
H2CB-4-G9-IGFR	WAGGSDVDGSFYDWFRQLLAS	21.6	14.5	15.2	1.1
H2CB-3-C8-IGFR	GLQNVSFHSGFYEWFAQQVSQ	20.8	13.4	13.9	1.0
H2CB-3-A12-IGFR	SRVSDPYHVGFYQWFEFVRG	28.6	27.5	29.2	0.9
H2CB-3-B12-IGFR	MGGATFFHTGFDWFAAQLQH	27.8	25.2	27.1	0.9
H2CB-3-A9-IGFR	RPASRPFHSGFYQWFAADQLSH	27.7	24.3	25.7	0.9
H2CB-3-A3-IGFR	GLAPGNFHEDFYRWFOEQTLG	26.9	24.1	26.5	0.9
H2CB-3-B4-IGFR	TAAISDFNSLFYGWFEQLLSS	25.8	23.8	25.3	0.9
H2CB-4-E7-IGFR	LDEDLPQHAGFYGWFAEALGV	24.6	21.6	24.0	0.9
H2CB-4-G6-IGFR	ASHKSAFDDNFYRWFSMQLRD	22.4	21.1	23.0	0.9
H2CB-4-E9-IGFR	HTGAGDLHGAFYNWFLEQLGG	24.3	20.7	22.0	0.9
H2CB-4-H2-IGFR	RRGRDGFHGGFYDWFAAQLSD	21.6	20.2	21.9	0.9
H2CB-3-A10-IGFR	GNFREAFHADFYSWFERQLQS	24.3	19.9	21.5	0.9
H2CB-3-C4-IGFR	RDTLPAFHQHFYQWFEKQVSA	23.1	19.2	22.0	0.9
H2CB-3-B5-IGFR	ERETAAFGQAFYQWFRDQIAG	24.2	18.8	20.7	0.9
H2CB-4-G4-IGFR	WGECCGFYDWFDQLGWEP SH	21.7	18.7	21.2	0.9
H2CB-3-D9-IGFR	SLVAADLHEGFYGFWRFSQLGG	24.4	18.6	20.0	0.9
H2CB-3-C3-IGFR	TSEVGDFHAEFYSWFEIQLGR	20.3	18.4	21.1	0.9
H2CB-3-D3-IGFR	TGADGLLHARFYAWFEEQLRE	22.5	18.3	21.3	0.9
H2CB-4-F2-IGFR	RRSDSSLHRSFYDWFSVQLLN	18.0	16.8	18.3	0.9
	SESKYLLHSGFYGWFEAQLRG				

FIG. 1N-2

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Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	--
H2CB-4-H1-IGFR	XXXXXXXXXXFXWFXXXXXX	18.3	15.3	16.5	0.9	1.1	1.1
H2CB-4-F9-IGFR	HGVIRADHTGFGWFSKQLSD	22.9	14.4	15.3	0.9	1.1	1.1
H2CB-4-E10-IGFR	LINA.VFRRGFYAWFEEQVSK	26.1	20.1	24.5	0.8	1.2	1.2
H2CB-4-F8-IGFR	LQRYIGFHDPPFYDWFSAISG	21.5	14.8	19.0	0.8	1.3	1.3
H2CB-3-A8-IGFR	MRTAELFHVGFDYDWFDAQLMD	20.7	14.7	18.2	0.8	1.2	1.2
H2CB-4-F1-IGFR	WAPPDALHGQFYRWFORQLDQ	22.2	14.6	18.8	0.8	1.3	1.3
H2CB-3-C6-IGFR	AVHAATFHDDFYRWFEQVVG	15.7	7.8	10.2	0.8	1.3	1.3
H2CB-4-E11-IGFR	FDAVHGFDGGFYGWFKRELQR	26.1	17.6	24.1	0.7	1.4	1.4
H2CB-3-D6-IGFR	QAGMEFHGAFYNNWFLQQLSG	21.6	13.0	18.8	0.7	1.5	1.5
H2CB-4-F3-IGFR	GRSVSRMNAEFYQWFGHQLAA	17.3	11.1	16.4	0.7	1.5	1.5
H2CB-3-A4-IGFR	AAVNSLFHDEFYLVWFQDQLDG	27.4	11.0	14.8	0.7	1.3	1.3
H2CB-3-B1-IGFR	QLGMDWFHADFYEWFLAQLPS	20.0	11.0	15.2	0.7	1.4	1.4
H2CB-3-C5-IGFR	RLAGSGIHGFGYGFVFDQLLA	19.9	10.5	15.6	0.7	1.5	1.5
H2CB-4-F6-IGFR	GREIGGVHDGFDYDWFRRQSEQ	18.6	10.1	14.6	0.7	1.4	1.4
H2CB-3-B8-IGFR	VRSEQRDSSSFYQWFNDLLMS	20.7	6.9	9.5	0.7	1.4	1.4
H2CB-3-C7-IGFR	QSPYGFHHDGFYRWFLQQTGM	16.2	1.8	2.5	0.7	1.4	1.4
H2CB-4-H7-IGFR	FQCGAAPHVDYRWFTTCQEQF	21.8	14.1	22.7	0.6	1.6	1.6
H2CB-4-F5-IGFR	GAFGSEFHEQFYRWFEEDALSF	12.9	4.0	7.2	0.6	1.8	1.8
H2CB-4-G1-IGFR	EHTSYQIHRQFYEWFDRLGR	20.4	10.3	19.7	0.5	1.9	1.9
H2CB-3-D11-IGFR	SGTAADLHSRFYGFALQARE	24.1	8.8	18.6	0.5	2.1	2.1
H2CB-3-D7-IGFR	EGFVLPHGQFYRWFLQLLDG	22.1	6.5	13.6	0.5	2.1	2.1
H2CB-3-C10-IGFR	QOSAGHPHSSFYLWFESELLGA	21.7	5.1	10.4	0.5	2.0	2.0
H2CB-4-E3-IGFR	YLQAGFHRSFYGFEDQALRD	20.3	4.6	8.9	0.5	1.9	1.9
H2CB-3-C1-IGFR	MWLWATLHSDFYSWFEQVVG	22.3	6.7	15.7	0.4	2.3	2.3
H2CB-4-G2-IGFR	GANALGFKDRFYEWFAAQLWD	19.9	3.3	10.7	0.3	3.3	3.3
H2CB-3-A11-IGFR	GSGLYVFHWGFDYDWFEEQMG	23.9	2.5	7.7	0.3	3.1	3.1
H2CB-4-G5-IGFR	LDKGWGFDLQFYRWFEAATRA	19.3	2.5	7.9	0.3	3.1	3.1
H2CB-4-F12-IGFR	QRSVEFHADFYDWFRLRLTP	16.7	1.7	5.4	0.3	3.1	3.1
	DQRMGSFHGEFYRWFEETLLS						

FIG. 1N-3

Clone Design	Sequence X _n -Fy _x WE-X _n	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	--
20E2A-3-B11-IR	GRFYGWFDQDAIDQLMPWGFDP	24.6	1.4	23.6	0.1	16.8	--
20E2Bβ-3-E3-IR	IQWEPFYGWFDVVAQMFE	23.0	0.9	15.3	0.1	16.3	--
rB6-3-F6-IR	RYGRWGLAQQFYDWFDR	40.9	1.0	13.3	0.1	13.3	--
rB6-4-F9-IR	RRLGSLSTQFYNWFAE	34.1	1.0	12.6	0.1	12.6	--
20E2Bα-3-A8-IR	ASAYTPFYQWFADVVSEYMQQ	35.4	7.4	34.4	0.2	4.6	--
A6L-4-F6-IR	PYRMETKWNFYDWFVAQLQ	28.9	4.1	18.1	0.2	4.4	--
20E2Bα-4-H9-IR	SAVHFQFYKWFNDLLPVPLSA	37.8	9.4	26.7	0.4	2.9	--
20E2Bα-3-B1-IR	VPVNKSFYRWFLVLGGSDDW	41.8	12.9	36.8	0.4	2.9	--
20E2Bβ-4-F9-IR	QSPRASFYGWFDVLRAGVV	25.9	4.2	10.1	0.4	2.4	--
20E2Bβ-3-E9-IR	TGFYEWFYEQ _L HSRMLPNPLD	27.0	7.7	17.2	0.5	2.2	--
20E2Bβ-3-E10-IR	RRGVGGFYGWFSQ _L LQGMGVA	22.2	2.6	5.5	0.5	2.1	--
20E2Bα-3-C12-IR	SSQDRRFYRWFEQAIVGGRDG	39.0	6.7	12.0	0.6	1.8	--
20E2Bβ-3-C12-IR	TRGQLGFYNWFQ _L ALSTSGMG	20.2	2.2	3.8	0.6	1.8	--
20E2Bβ-3-E7-IR	CADLNAFYQWFCGVLD _R SGDH	9.2	1.2	1.9	0.6	1.6	--
20E2Bβ-3-E11-IR	TLIQDQFYWWFS _D LLSAEPGD	20.7	1.3	2.1	0.6	1.6	--
20E2Bα-3-B11-IR	IDQLDAFYRWFDGVM _L GMGDP	36.0	20.7	32.8	0.6	1.6	--
NNKH-4-G2-IR	RGGGTFYEWFE _S ALRKHGAG	10.8	6.3	8.9	0.7	1.4	--
20E2Bα-3-A7-IR	RGLDQDFYRW _F QNLV _G VEYDR	19.0	4.2	5.5	0.8	1.3	--
20E2Bα-4-G12-IR	MQHGRGFYGW _F ARVLEQ _D DRGW	37.0	22.3	29.5	0.8	1.3	--
20E2Bα-3-C11-IR	ERLHLRFYEW _F DTVIG _D QGS	37.3	26.8	34.8	0.8	1.3	--
20E2Bα-3-C10-IR	MHVQSDFYHWF _S LLG _G QGGPD	37.7	24.8	30.5	0.8	1.2	--

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FIG. 10-1

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Clone Design	Sequence X_n -Fy x WF- X_n	Ratios over Background			Comparisons	
		E-Tag --	IGFsR --	IR --	IGFR/IR --	IR/IGFR --
20E2B α -3-D7-IR	TMGTQGFYRWFQNVVKEHLSG	35.4	26.9	31.3	0.9	1.2
20E2B α -3-A12-IR	ITHNRGFYSWFDDVVQGGAGA	31.7	22.0	23.3	0.9	1.1
20E2B α -3-D10-IR	VRRDAGFYQWFADILTQLDFE	32.7	27.3	29.1	0.9	1.1
20E2B α -4-G7-IR	MQLQDEFYNWFRGIMLNDGQD	34.2	29.0	30.7	0.9	1.1
20E2B α -4-F5-IR	GIRSSGFYQWFDRLVLAGVGDG	33.8	32.1	34.0	0.9	1.1
20E2B α -3-C9-IR	ANLNSQFYSWFASVTGEASPS	39.4	33.2	35.5	0.9	1.1
20E2B α -3-A4-IR	QSPRASFGWFDDVLRAGVV	38.2	31.6	35.9	0.9	1.1
20E2B α -4-E12-IR	MQRNQGFSWFDDLVSSTVGV	36.0	30.8	29.7	1.0	1.0
20E2B α -4-E11-IR	ASGFDPFYAWFLEQLRVANGS	35.1	31.2	30.7	1.0	1.0
20E2B α -4-E8-IR	SGTPYGFYRWFQSALASATSG	36.1	30.5	30.7	1.0	1.0
20E2B α -4-H10-IR	QGVEGGFYWFDRAMGDVRPW	38.9	30.6	30.7	1.0	1.0
20E2B α -4-F6-IR	DNMSGGFYRWFQVVADSGGD	34.9	33.2	32.0	1.0	1.0
20E2B α -4-G4-IR	RGTDDTFYGWFDQLLQGCDD	34.1	33.7	32.2	1.0	1.0
20E2B α -4-F8-IR	TVDHTQFYDWFSSRVLGESGA	37.7	32.0	32.7	1.0	1.0
20E2B α -4-G5-IR	GRQDREFYWFELQAGGMDGD	34.9	33.9	33.4	1.0	1.0
20E2B α -3-B10-IR	RLLGGFYWFQVLKETKEV	38.2	34.9	33.6	1.0	1.0
20E2B α -3-C7-IR	GVLSTGFYWFALQLHGLAAG	37.6	34.2	34.8	1.0	1.0
20E2B α -3-C5-IR	PAVGQSFYGFWEAVLRGSKAG	40.4	36.0	35.6	1.0	1.0
20E2B α -3-B9-IR	SNGISGFYWFQAAQVQTSDFQ	39.6	35.8	37.1	1.0	1.0
A6L-4-F11-IR	LLGLSQAAAYANFYDWFVSQLA	33.1	4.6	4.6	1.0	1.0
	VPNSWMFYNWFAEQIEGSEGE	44.1	40.0	38.1	1.0	1.0
20E2B α -3-C2-IR	ARRADGFYDFREQVSGSAVQ	43.1	40.1	39.0	1.0	1.0
20E2B α -3-B2-IR	GWVEGTFYWFDRLLGGVQGD	34.1	33.6	29.8	1.1	0.9
20E2B α -4-G2-IR	SHLTDPFYQWFVDQLRAGVRG	39.4	36.0	31.9	1.1	0.9

FIG. 10-2

Clone Design	Sequence X_n -Fy x WF- X_n	Ratios over Background			Comparisons		
		E-Tag --	IGF ₃ R --	IR --	IGFR/IR --	IR/IGFR --	34/122
20E2B α -4-H5-IR	RSNDDAFYRWFSN \bar{I} LQVDGGG	38.7	35.1	32.3	1.1	0.9	
20E2B α -4-G3-IR	DSDGAQFYIWFEDQLRSAGWD	35.5	36.1	32.7	1.1	0.9	
20E2B α -4-H4-IR	PGLHRAFYQWF \bar{A} EAVRSANKE	38.8	37.9	35.0	1.1	0.9	
20E2B α -3-C1-IR	SLGQGGFYDWFASQVGGADI	43.7	42.1	39.0	1.1	0.9	
20E2B α -4-E6-IR	CGQTQSFYQWFCEVMRVE \bar{S} GD	38.0	34.3	29.7	1.2	0.9	
H5-3-D5-IR	IVVPGDTQGVNFYDWFVKQLQ	43.8	21.8	18.2	1.2	0.8	
JBA5-3-D9-IR	RDVSMGSASTNFYDWFVQQLG	38.3	29.8	25.3	1.2	0.8	
20E2B β -4-G6-IR	SQAGSAFYAWFDQVLR \bar{T} VHSA	22.4	6.2	1.9	3.3	0.3	
20E2B β -4-H10-IR	SNGISGFYEWFAAQVQ \bar{T} SDFQ	23.5	32.2	9.7	3.3	0.3	
IB6-4-G8-IR	RRDRGGLDVFFYQWFMD	--	--	--	--	--	

FIG. 10-3

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Ratios over Background		Comparisons	
E-Tag	IGF _s R	IGFR/IR	IR/IGFR
--	--	--	--
39.1	1.8	27.7	15.4

Sequence
xxxxxxxxxxxxxxxxxxxx
HLCVLEELFWGASLFGYCSG

Clone
Design
R20β-4-F8-IR

FIG. 2A

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF ₃ R	IR	IGFR/IR
F815-4-H9-IR	HLCVLEELFWGASLFGYCSCG	--	--	--	--
F815-3-B1-IR	PLCVLEELFWSTPLFGQCSY	34.9	0.9	37.6	<0.1
F815-3-D1-IR	HLCVLEELFWGASLFAQCVG	31.7	0.9	35.8	<0.1
F815-3-D4-IR	DLCVLEELFWGASRFGQCSG	30.4	0.9	33.5	<0.1
F815-3-C5-IR	HLCVLEELFWGASLFGQCAG	31.5	0.9	33.6	<0.1
F815-4-H3-IR	HLCVVEELFWGASLFGQCSG	31.1	0.8	31.2	<0.1
F815-3-A5-IR	NLCDLEVLFWGASLFRQCSG	33.7	1.0	37.2	<0.1
F815-3-D7-IR	PLCVLEEQFWGASLFGQCSG	37.4	1.1	40.9	<0.1
F815-3-A1-IR	QLCVLEELFWGASEFGQCSG	33.6	0.9	34.3	<0.1
F815-4-H4-IR	HLCVLEELFWGASLFGQCSG	29.8	0.9	34.8	<0.1
F815-3-A3-IR	PLCVLEELFWGESLFGQCSG	31.1	0.9	32.7	<0.1
F815-3-B3-IR	HLCVLEELFWGASRFGQCSG	32.8	1.0	39.1	<0.1
F815-3-A4-IR	KLCVLEELFWGASLFGQCSG	33.7	1.0	37.5	<0.1
F815-3-D2-IR	YLCVLEELSWGASLFGQCSG	32.5	1.0	36.9	<0.1
F815-3-C4-IR	HLCVLEELWGASLFAQCSG	31.9	0.9	34.1	<0.1
F815-3-B4-IR	QLCVLEQLFWGESLFGQCSG	31.6	0.8	31.8	<0.1
F815-3-C1-IR	HLCVLEELFWGGLFSQCSG	33.8	1.0	36.7	<0.1
F815-4-G9-IR	HLCVLEELFWGASLYGQCSG	29.0	0.9	35.0	<0.1
F815-4-G6-IR	SICALEEQFWGAALFGYCSCG	36.5	1.0	38.9	<0.1
F815-3-A8-IR	HLCVLEEQFWGASLFDGCAG	34.9	1.0	36.4	<0.1
F815-4-G5-IR	QLCVLEELFWGASLFGQCSG	34.7	1.1	39.3	<0.1
F815-3-B5-IR	PLCVLEELFWGAALFGQCSG	26.5	1.0	35.1	<0.1
F815-4-F4-IR	HLCVLEELFWGASLFGQCTG	33.2	0.9	34.1	<0.1
F815-3-A2-IR	PLCVLEELFWGSLFGQCSG	28.6	0.8	30.0	<0.1
F815-3-B6-IR	QLCVLEELVWGASLFGQCSG	32.5	1.0	36.6	<0.1
F815-4-H7-IR	HLCVVEELVWGASLFGQCSR	31.6	0.9	32.9	<0.1
F815-4-H8-IR	DLCVLEELFWGASLFGQCAG	33.7	1.0	37.6	<0.1
F815-4-G7-IR	QLCVLEERFWGASLFGQCSG	35.8	1.0	37.0	<0.1
	NLCVLEELFWGAALFGQCSG	33.7	1.0	35.8	<0.1

FIG. 2B-1

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Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	IR/IGFR
F815-3-A6-IR	HLCVLEELFWGASLFGYCSCG	34.6	1.1	39.0	<0.1	--	36.2
F815-3-D3-IR	QLCVLEELFWGSSLFGQCSCG	33.8	1.0	36.2	<0.1	--	36.2
F815-3-B12-IR	DLCVVEELFWGKSLFGQCSCG	33.2	1.0	35.7	<0.1	--	36.2
F815-4-G10-IR	DLCVLEELFWGSSLFGQCSCG	35.4	1.0	37.2	<0.1	--	36.1
F815-4-E3-IR	YLCVLEEQFWGASLFRQCFG	32.4	1.0	35.0	<0.1	--	36.1
F815-4-E6-IR	HLCVLEELWGSSLFGQCSCG	33.2	1.0	34.5	<0.1	--	36.1
F815-4-F1-IR	PLCGLEELFWGASLFGQCSD	29.4	0.9	32.5	<0.1	--	36.0
F815-4-G8-IR	HLCVLEELFWGSSLFAQCSCG	36.8	1.1	38.2	<0.1	--	35.9
F815-4-H12-IR	PLCAIEELFWGAALFGQCSCG	30.5	0.9	31.9	<0.1	--	35.9
F815-4-G3-IR	HLCVLEEQFWGASLFGDCSG	31.4	1.0	35.7	<0.1	--	35.7
F815-3-C2-IR	PLCVLEELFWGAPLFGQCSD	32.3	1.0	36.1	<0.1	--	35.6
F815-4-E10-IR	DLCGLEELFWGAALFGQCTS	35.4	1.0	36.5	<0.1	--	35.4
F815-3-A12-IR	QLCVLEKQWGLASLFWQCSCG	32.1	1.0	36.3	<0.1	--	35.3
F815-3-B8-IR	HLCVLEELFWGASLYGQCPG	33.6	1.0	35.8	<0.1	--	35.3
F815-3-B2-IR	HLCVLEELFWGASLFDQCSCG	31.0	1.0	35.3	<0.1	--	35.3
F815-3-B2-IR	HLCVLEELWGLASLFGQCSCG	30.1	1.0	35.3	<0.1	--	35.3
F815-3-C3-IR	PLCVLEELFWGVSLFGQCGG	33.1	1.0	35.8	<0.1	--	35.2
F815-3-A7-IR	HLCVLEELFWGASQWGCSCG	33.4	1.0	35.7	<0.1	--	35.2
F815-4-F9-IR	RLCVLEEQFWGGALFGQCSCG	32.0	1.0	33.5	<0.1	--	35.0
F815-3-B7-IR	QLCVLEELFWGVSLFAQCSCG	28.0	1.0	33.4	<0.1	--	35.0
F815-4-E4-IR	HLCVLEELFWGAALFGQCFG	28.0	0.9	30.2	<0.1	--	34.8
F815-4-E12-IR	YLCVLEELFWGASQFGQCSCG	33.8	1.0	35.2	<0.1	--	34.7
F815-4-F8-IR	HLCVLEELYWGLASLFGQCSCG	33.9	1.0	34.7	<0.1	--	34.7
F815-3-C7-IR	HLCVLEERFWGVSLFGQCSCG	32.7	1.0	34.2	<0.1	--	34.7
F815-4-F10-IR	PLCVLEELFWGASRFGQCSCG	35.4	1.1	37.3	<0.1	--	34.6
F815-3-D11-IR	HLCVLEDLFWGASLFDQCSCG	30.3	0.9	32.2	<0.1	--	34.6
F815-4-E7-IR	HLCVLELVFWGASLFGQCSCG	34.0	1.1	36.4	<0.1	--	34.3
F815-3-A10-IR	QLCVLEELFWGTSLFGYCSCG	33.7	1.1	36.3	<0.1	--	34.2
F815-3-B11-IR	ALCVLEELFWGESLFGQCSCG						

FIG. 2B-2

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR
F815-4-F11-IR	HLCVLEELFWGASLFGYCSG	31.8	1.0	33.7	<0.1
F815-3-A9-IR	RLCVLEERFWGAALFGQCSG	31.9	1.0	35.5	<0.1
F815-4-G11-IR	PLCVLEELFWGASLFGQCSG	32.3	1.0	34.4	<0.1
F815-3-D8-IR	SLCVLEELFWGSRFGQCSG	32.3	1.0	33.3	<0.1
F815-4-G4-IR	HLCVLEEQFWGASLFGQCSG	23.8	1.0	32.2	<0.1
F815-3-C8-IR	DLCLLEELLWGASRFGQCSG	33.9	1.0	35.1	<0.1
F815-4-G12-IR	YLCVLEERFWGASLFGQCSG	31.7	1.0	33.5	<0.1
F815-3-D12-IR	HLCVLEEQFWGASLFGSCSG	33.3	1.0	34.8	<0.1
F815-4-F7-IR	QLCVLEEQLWGASLFGQCSG	33.3	1.0	34.3	<0.1
F815-4-F2-IR	HLCVLEELF*GESLFGYCSG	26.1	1.0	33.8	<0.1
F815-3-B9-IR	HLCVLEELFWGASLFGQCSG	33.6	1.1	35.7	<0.1
F815-4-H2-IR	PLCVLEELFWGASHFGQCSG	36.1	1.2	38.4	<0.1
F815-4-E11-IR	HLCVLEELVWGASLFGQCSG	33.2	1.1	35.4	<0.1
F815-4-G1-IR	QLCVLEELVWGASLFGQCSG	27.9	1.0	31.5	<0.1
F815-3-A11-IR	HLCVLEELFWGASLFGQCSG	37.7	1.2	40.1	<0.1
F815-4-F6-IR	HLCVLEELVWGESLFGQCSG	32.3	1.1	34.6	<0.1
F815-3-D9-IR	RLCVLEELYWGASLFGQCSG	31.4	1.0	32.5	<0.1
F815-3-C11-IR	RLCILEELFWGASLFGQCSG	33.4	1.1	35.7	<0.1
F815-4-G2-IR	HLCVLEELFWGATLFDQCSG	30.2	1.1	34.3	<0.1
F815-3-C9-IR	HLCFLEELFWGASLFGQCSG	29.7	1.0	31.4	<0.1
F815-4-H10-IR	HLCIVEELFWAAPLFGQCSG	31.9	0.9	27.6	<0.1
F815-4-F3-IR	HLCVLEELVWGASLFAQCSA	19.4	1.0	28.0	<0.1
F815-4-F5-IR	NLCVLEELFWGASQFRYCPG	12.3	0.9	24.8	<0.1
F815-4-H1-IR	RLCVLEELFWGASLFGQCSG	6.9	1.0	15.8	0.1
F815-4-E5-IR	PLCVLEELFWGASLFGQCPG	3.5	1.0	13.6	0.1
F815-4-H5-IR	NLCVLEELFWGASLFGQCSG	5.5	1.0	13.1	0.1
F815-3-C10-IR	QLCVLG#RFWGGSLCGYCSG	3.5	1.1	5.2	0.2

FIG. 2B-3

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR
			39.1	1.8	27.7	0.1	15.4
		HLCVLEELFWGASLFGYC SG					
	F815-4-F11-IGFR	PLCFLQELFGGASLGGYC SG	33.4	12.3	1.0	12.3	0.1
	F815-4-E12-IGFR	FMCGLQELVGGAAALLGHCS G	33.7	15.1	1.7	8.9	0.1
	F815-4-H10-IGFR	PLCFLQELFGGSLSGYC SG	30.1	8.5	1.0	8.5	0.1
	F815-4-B7-IGFR	FLCGLEELAWGVSRS GYC FG	35.2	23.9	4.8	5.0	0.2
	F815-3-B5-IGFR	PLCFLAELFSGSALGGDC SR	33.9	4.8	1.0	4.8	0.2
	F815-4-D12-IGFR	PLCVLQELFGGSLGGYC SG	33.6	7.0	1.8	3.9	0.3
	F815-4-C11-IGFR	QLCVLE#LFWGACLF GYC AG	13.9	4.6	1.8	2.6	0.4
	F815-4-C7-IGFR	FLCGLQELSGVASLFGQ CSG	16.8	2.0	1.0	2.0	0.5
	F815-4-E7-IGFR	RVCVLEQLVWGASLFGA* SG	26.9	3.8	1.9	2.0	0.5
	F815-4-G7-IGFR	FYCGLEELSWGAA LFG YC SG	30.4	9.0	5.0	1.8	0.6
	F815-4-A10-IGFR	FLCGLEELSQQAVLFG H CYG	30.8	3.7	2.2	1.7	0.6
	F815-3-B3-IGFR	HLCVLVGLFWDASLFGQ CSG	7.6	1.0	2.0	0.5	2.0
	F815-3-G1-IGFR	QRCIRAALFWCATLLGG CAG	20.5	1.0	2.0	0.5	2.0
	F815-4-G12-IGFR	HQCI P DGMSQGAALRG NC SD	7.6	1.0	2.5	0.4	2.5
	F815-3-H1-IGFR	HLCVLEDELWGVSLFGYC SS	18.4	1.0	6.8	0.1	6.8

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FIG. 2C

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons		
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR	IR/IGFR
		<u>HLCVLEELFWGASLFGYCSCG</u>	39.1	1.8	27.7	0.1	0.1	15.4
		HLCMLEEQFWGASLFSRCSG	28.1	0.9	17.9	<0.1	<0.1	21.1
		TCAFWKNGSVRRCSVTAVV	34.0	1.6	22.7	0.1	0.1	13.9
		PLCGLKN.SGVRLCSSPALV	21.3	0.7	9.0	0.1	0.1	13.4
		PLCLQEELFWGASLFGYCSCG	34.1	1.0	12.1	0.1	0.1	12.1
		PLCDLEELFWGASLFGDCPG	14.2	0.6	6.5	0.1	0.1	11.6
		DLCVLEELFWDGSLFASCSG	14.0	0.5	6.1	0.1	0.1	11.5
		PLCVLEELWGTALFGSCTG	38.1	1.2	11.8	0.1	0.1	9.9
		PLCLVEELWGASLFSQCTG	15.1	0.7	6.4	0.1	0.1	8.7
		PLCDLEELYWGAALFGSCSG	46.3	2.7	22.2	0.1	0.1	8.2
		GLCFLEEQFWGTSLFRDCPG	14.5	0.6	4.7	0.1	0.1	8.0
		PLCVVEELFWGASLYGQCSG	8.8	0.6	4.4	0.1	0.1	7.5
		RLCVLEELFWGASRFRGCSG	11.7	0.6	4.2	0.1	0.1	7.4
		PLCVLEELHWGAALFGYCSCG	16.0	0.6	4.7	0.1	0.1	7.3
		NLCVVEELFWGASLFPNCSG	14.5	0.8	5.9	0.1	0.1	7.1
		QLCVLEELFWGASMFEDCSG	5.0	0.4	2.4	0.2	0.2	6.9
		HLCVLEEQFWGASLFGQCSG	37.5	1.1	7.5	0.2	0.2	6.6
		PLCVLEEIYWGAALFGDCYG	21.2	1.1	6.4	0.2	0.2	5.9
		PLCVLEELFWGLSLDKNCS	7.5	0.7	3.7	0.2	0.2	5.6
		QLCVLEELFWGASLFSGCSG	5.3	0.8	4.4	0.2	0.2	5.2
		PLCDLEALFWGESLFGGCSG	5.7	0.6	3.0	0.2	0.2	4.9
		HLCVLEEMFWGTSHFDGCSG	9.1	1.0	4.7	0.2	0.2	4.7
		DLCVLEELFWGAPLFGLCSCG	5.9	0.8	3.5	0.2	0.2	4.5
		DLCVLEELFWGVALYGGCSG	25.7	2.3	10.5	0.2	0.2	4.5
		QLCVLEELYWGASLFGHCSG	3.7	0.6	2.7	0.2	0.2	4.2
		HLCVLEDRFWGASLFGPCSG	11.3	0.6	2.2	0.3	0.3	3.5
		HLCGMEEMFWGVALFRNCSG	7.6	0.8	2.7	0.3	0.3	3.5
		PLCVLEQLYWGESLFFVYCSG	8.0	1.2	4.3	0.3	0.3	3.5
		HLCVLEELFWGEALWGYCSG	17.5	2.6	9.0	0.3	0.3	3.4

FIG. 2D-1

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Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag --	IGF3R --	IR --	IGFR/IR -- IR/IGFR --
F820-4-A8-IR	HLCVLEELFWGASLFGYCSCG	6.4	0.7	2.4	0.3 3.4
F820-4-G1-IR	QLCVMEELFWGASRFGQCSG	3.9	0.6	1.9	0.3 3.4
F820-4-F3-IR	HLCVLEELFWGASMFQCSG	9.8	1.3	3.6	0.4 2.9
F820-4-D6-IR	QLCVLEEMFWGSRFVQCSA	5.4	1.2	3.2	0.4 2.6
F820-4-A1-IR	PLCILEELFWGEALFDQCGA	25.5	2.4	6.1	0.4 2.5
F820-4-H2-IR	YLCVQEELFWGASLFGYCSV	15.9	1.6	4.1	0.4 2.5
F820-4-F4-IR	HLCALAEAFFGPSLFNSCQG	6.8	1.9	4.7	0.4 2.5
F820-4-B6-IR	HLCVLEERFWGASLFGQCSG	4.1	0.8	1.9	0.4 2.4
F820-4-B11-IR	QLCDLEELFWGASLFGYCPG	22.2	3.1	7.0	0.4 2.3
F820-4-H6-IR	HLCVLEERFWGASIWGSCSG	4.1	1.1	2.4	0.5 2.2
F820-4-H9-IR	QLCVLEELFWGSLWGQCSR	3.1	0.9	1.9	0.5 2.1
F820-4-D3-IR	PLCVLEELFWGAAQFGQCSG	4.6	1.3	2.5	0.5 1.9
F820-4-C1-IR	QLCDLEERFWGVSLFGLCSG	13.0	1.1	2.1	0.5 1.9
F820-4-D12-IR	QLCVLEEVFWGASLFGICTG	10.4	1.2	2.0	0.6 1.7
F820-4-B8-IR	QL.DLNTWSGLCLCSVTVRV	7.2	2.2	3.4	0.6 1.5
F820-4-C6-IR	DLCVLEESLWGKALFGYCSD	13.9	2.5	2.8	0.9 1.1
F820-4-C10-IR	HLCVLEEVFWGSSMFGDCSG	5.3	2.6	2.9	0.9 1.1
F820-4-D4-IR	HLCDLEELFWGASLFGDCQG	3.5	2.3	2.1	1.1 0.9
F820-4-E1-IR	QLCVLDALMWGGCRLGHQCG	1.6	1.6	1.5	1.1 0.9
F820-4-B3-IR	QLCVLEEKFWGTSLFGDCMG	15.9	0.6	5.0	1.2 0.8
F820-4-D2-IR	HLCVLEEVFWGAAQFGSCSG	7.8	3.2	2.5	1.3 0.8
F820-4-C5-IR	QLCVLEELFWGSPMFGYCSG	21.5	4.0	2.3	1.8 0.6
	HLCDLEELFWGASGFAQCYG				

FIG. 2D-2

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Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
A6L-3-C4-IR	<u>HLCVLEELFWGASLFGYC</u> SG	--	--	--	--	--
A6L-3-D7-IR	DLCVLEERFWGASLFGQCSG	36.9	1.0	40.5	<0.1	42.5
A6L-3-A1-IR	QLCVLEELHWGASLFGYC	38.6	1.0	40.1	<0.1	40.7
A6L-3-C1-IR	PLCVLEEQFWGASLFGQCSG	39.6	1.1	44.8	<0.1	40.6
A6L-3-D5-IR	YLCDLEERFWGASLFGQCS	37.3	1.0	40.3	<0.1	40.3
A6L-3-A4-IR	HLCVLEELFWGASQFGFC	42.9	1.1	44.4	<0.1	40.2
A6L-3-D3-IR	HLCVLEELFWGASLFGQCSG	26.7	1.1	42.2	<0.1	40.2
A6L-3-B1-IR	HLCVLEERFWGASLFGQCSG	34.6	0.9	36.9	<0.1	39.8
A6L-3-B5-IR	HLCVMEELFWGTSLFGQCTG	33.9	1.0	38.7	<0.1	39.3
A6L-3-B2-IR	HLCVLEERFWGASLFGQCSG	35.3	1.1	42.4	<0.1	38.6
B6H-4-G12-IR	HLCVLEERFWGASLFSQCSG	38.1	1.1	42.7	<0.1	37.7
B6C-4-H10-IR	HLCVLEELFWGASLFGQCSG	31.6	1.1	39.6	<0.1	36.7
B6H-4-G8-IR	QLCVLEELFWGAASFGQCSG	38.5	1.1	41.1	<0.1	36.5
A6L-3-D6-IR	HLCVLEEMFWGASLFGQCSG	31.7	1.1	39.7	<0.1	36.2
B6C-4-F1-IR	HLCVLEELFWGASLFGQCSR	35.5	1.0	37.2	<0.1	36.1
B6C-4-H3-IR	QLCVLEELFWGASQFGYC	32.9	1.1	38.7	<0.1	35.8
B6H-4-E8-IR	QLCALEEQFWGASLFSQCSG	37.4	1.2	40.5	<0.1	34.8
B6C-4-G1-IR	QLCVLEELFWGASLFGYC	30.2	1.0	35.7	<0.1	34.3
B6H-4-E9-IR	HLCVLEEWFGDSLFGQCSR	34.9	1.2	40.2	<0.1	33.7
B6C-4-F5-IR	HLCVLEERFWGASLFGQCSG	34.4	1.2	38.8	<0.1	33.2
B6C-4-F11-IR	QLCELEEVFWGASLFDYC	34.7	1.2	39.6	<0.1	32.8
B6C-4-E6-IR	HLCVLEELFWGASLFGQCSG	34.0	1.2	37.2	<0.1	31.7
B6C-4-E12-IR	HLCVLEELFWGASLFGQCSA	32.3	1.2	37.4	<0.1	30.6
B6C-4-G10-IR	HLCVLEELIWGASRFGQCSG	30.9	1.1	33.3	<0.1	30.2
B6C-4-F8-IR	HLCVLEELFWGSLFIQCSG	33.0	1.3	40.3	<0.1	30.1
20C-3-B5-IR	QLCVLEEQFWGASLFGNC	36.4	1.4	39.8	<0.1	29.3
B6C-4-G3-IR	HLCVLEERFWGAALFGQCSG	26.6	1.1	32.5	<0.1	29.2
20C-3-B7-IR	HLCVLEEMFWGASLFGQCGG	34.0	1.4	38.8	<0.1	28.3
	PLCVLEELVWGASLFGQCSG	29.5	1.2	32.9	<0.1	28.3

FIG. 2E-1

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20C-3-B4-IR	HLCVLEELFWGASLFGYCSG	28.9	1.1	31.1	--
20C-3-C11-IR	NLCVLEELFWGESLFGQCSG	30.2	1.1	31.0	<0.1
B6C-4-G2-IR	HLCVLEEQFWGGSIFGYCSR	29.4	1.3	35.3	<0.1
20C-3-B8-IR	HLCFLEEVFWGAALFAQCSG	28.5	1.1	31.2	<0.1
20C-3-C10-IR	HLCDLELVFWGSALFGQCSG	32.1	1.2	33.6	<0.1
20C-3-B6-IR	HLCVMEELFWGASLFGQCSG	29.7	1.2	31.9	<0.1
A6L-3-A3-IR	HLCVLEEQYWGESLFGYCSG	14.4	1.1	28.3	<0.1
A6L-3-B3-IR	PLCVLEEQFWGASLFAVCSS	38.7	1.7	43.4	<0.1
20C-3-A5-IR	QLCVLEELFWGESLFAQCLG	22.9	1.1	27.6	<0.1
20C-3-B11-IR	HLCVLEELFWGQSLFGHCSD	30.0	1.3	32.7	<0.1
20C-3-B3-IR	HLCVLEELVWGASLFGFCSG	29.3	1.2	31.2	<0.1
20C-3-C12-IR	LLCVLEEQFWGASLFGQCSG	29.6	1.3	31.8	<0.1
20C-3-C3-IR	RLCVLEELFWGESLFGQCSG	30.1	1.2	30.1	<0.1
20C-3-C2-IR	HLCVLEEMFWGASLFGNCSG	29.9	1.3	29.8	<0.1
20C-3-A11-IR	ELCFLEELFWGASLFGQCSG	25.9	1.2	27.4	<0.1
20C-3-A4-IR	HLCVLEELFWGASLYGQCSS	27.2	1.2	27.5	<0.1
20C-3-A6-IR	HLCVLEELFWGASLFAQCPG	26.1	1.2	27.5	<0.1
B6C-4-E4-IR	NLCVLEELFWGASEFGQCSG	34.5	1.7	39.1	<0.1
20C-3-A9-IR	DLCVLEEQIWGASLFRYCSG	29.7	1.3	29.3	<0.1
B6C-3-C5-IR	HLCVLEEQFWGVALFGNCSG	33.5	1.7	37.7	<0.1
20C-3-B1-IR	HLCVLEEQIWGASLFGQCSG	30.2	1.2	26.7	<0.1
20C-3-A10-IR	HLCVLEERFWGGALFGQCTA	29.0	1.3	28.5	<0.1
20C-4-F1-IR	HLCDLEELFWGASLFGQCSG	29.1	1.4	29.5	<0.1
20C-4-E1-IR	QLCVLEELFWGTSIFAGCSG	28.3	1.4	29.7	<0.1
20C-3-B12-IR	QLCGLEELFWGASLFGYCSA	27.0	1.3	25.8	<0.1
20C-3-A8-IR	HLCVLEELFWGASLFGQCSS	21.1	1.1	21.2	0.1
20C-3-A7-IR	FLCVLEELYWGASQFGQCSG	21.9	1.3	23.0	0.1
B6C-4-E10-IR	HLCVLEEQFWGASLFGYCSG	35.2	2.2	38.0	0.1

FIG. 2E-2

Clone Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
20C-3-A1-IR	HLCVLEELFWGASLFGYC <u>S</u> G	--	--	--	--	--
20C-3-C1-IR	RLCALEELFWGASLFGQ <u>C</u> SG	21.0	1.1	17.6	0.1	16.6
A6L-3-D2-IR	HLCVLEELFWGAALFHQ <u>C</u> SG	30.6	1.4	21.9	0.1	16.1
B6C-4-G12-IR	RLCVLEEQFWGASLFGQ <u>C</u> SG	7.0	1.1	14.9	0.1	14.1
B6H-4-F9-IR	QLCVLEELFWGSSRLGYC <u>S</u> G	31.1	2.5	33.5	0.1	13.6
B6C-4-E3-IR	DLCVLEELFWGASLFGQ <u>C</u> SG	39.3	3.6	43.1	0.1	12.1
20C-3-B10-IR	QLCLLEEQFWGGS ¹ LFGQ <u>C</u> SG	34.6	5.3	40.0	0.1	7.6
20C-3-A3-IR	HLCVLEELFWGTS ¹ LFGQ <u>C</u> SG	29.9	16.9	31.7	0.5	1.9
	RLCVLEELVWGASLFDQ <u>C</u> SR	28.4	19.1	25.3	0.8	1.3

FIG. 2E-3

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Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
D815-4-A8-IR	WLDQEWAWVQCEVYGRGCP	44.8	1.4	24.2	<0.1
D815-4-D10-IR	WLDLEWAQVQCEVYGRGCP	48.0	1.0	48.4	<0.1
D815-4-D9-IR	WLDQEWAWVQCEVYGRGCP	49.2	1.0	48.2	<0.1
D815-4-A11-IR	WLDQEWAWVQCEVYGRGCP	47.5	1.0	48.0	<0.1
D815-4-E12-IR	RLDEEWAWVQCEVYGRGCP	47.9	1.0	48.0	<0.1
D815-4-B7-IR	WLDQEWAWVQCEVYGRGCP	49.0	1.0	47.6	<0.1
D815-4-D11-IR	WLDQEWAWVQCEVYGRGCP	45.4	1.0	47.2	<0.1
D815-4-D12-IR	WLDQEWAWVQCEVYGRGCP	49.5	1.0	47.0	<0.1
D815-4-F8-IR	WLDQEWAWVQCEVYGRGCP	48.1	1.0	46.6	<0.1
D815-4-A9-IR	WLDQEWAWVQCEVYGRGCP	47.8	1.0	46.4	<0.1
D815-4-E9-IR	SLDQEWAWVQCEVYGRGCP	47.7	1.0	45.8	<0.1
D815-4-B10-IR	WLDQEWAWVQCEVYGRGCP	47.8	1.0	45.8	<0.1
D815-4-H8-IR	WLDQEWAWVQCEVYGRGCP	49.0	1.0	45.6	<0.1
D815-4-E10-IR	SLDQEWAWVQCEVYGRGCP	49.0	1.0	45.6	<0.1
D815-4-D7-IR	WLDQEWAWVQCEVYGRGCP	47.0	1.0	45.6	<0.1
D815-4-G9-IR	WLDQEWAWVQCEVYGRGCP	44.5	1.0	45.4	<0.1
D815-4-G12-IR	WLDQEWAWVQCEVYGRGCP	44.2	1.0	44.2	<0.1
D815-4-E11-IR	WLDQEWAWVQCEVYGRGCP	44.3	1.0	43.7	<0.1
D815-4-H7-IR	WLDQEWAWVQCEVYGRGCP	45.5	1.0	43.0	<0.1
D815-4-F12-IR	WLDQEWAWVQCEVYGRGCP	46.2	1.0	43.0	<0.1
D815-4-E8-IR	WLDQEWAWVQCEVYGRGCP	47.2	1.0	42.6	<0.1
D815-4-F9-IR	WLDQEWAWVQCEVYGRGCP	47.9	1.0	42.6	<0.1
D815-4-A10-IR	WLDQEWAWVQCEVYGRGCP	46.4	1.0	41.8	<0.1
D815-4-C7-IR	WLDQEWAWVQCEVYGRGCP	47.3	1.0	41.2	<0.1
D815-4-H10-IR	WLDQEWAWVQCEVYGRGCP	37.7	1.0	40.0	<0.1
D815-4-C9-IR	WLDQEWAWVQCEVYGRGCP	47.0	1.0	39.8	<0.1
D815-4-F11-IR	WLDQEWAWVQCEVYGRGCP	44.2	1.0	39.8	<0.1
D815-4-H12-IR	WLDQEWAWVQCEVYGRGCP	40.4	1.0	39.2	<0.1
D815-4-A7-IR	WLDQEWAWVQCEVYGRGCP	45.4	1.0	38.6	<0.1
D815-4-H11-IR	WLDQEWAWVQCEVYGRGCP	37.3	1.0	37.3	<0.1
D815-4-F7-IR	WLDQEWAWVQCEVYGRGCP	2.4	1.0	37.2	<0.1
		32.4	1.0	34.7	<0.1

FIG. 3B-1

Clone	Sequence
Parental/Design	<u>WLDQEWAWVQCEVYGRGCPS</u>
D815-4-G8-IR	<u>Q</u> LDQEWARVRCEVWGRGCSS
D815-4-G7-IR	WLDLEWAQVQCKVYGRGCPS
D815-4-G11-IR	WLDEEAWVQCQVYGRGCPS
D815-4-E7-IR	<u>WLDQEWAWVQCEVWGRGCAF</u>
D815-4-A12-IR	WLDREWAQVQCEVYGRGCLS
D815-4-B11-IR	WLD AE WEWVQCEVYGRGCRP
D815-4-D8-IR	SLDREWAYVQCQVYGRGCSS

Ratios over Background		Comparisons	
E-Tag	IGF3R	IR	IGFR/IR IR/IGFR
--	--	--	--
27.8	1.0	33.6	<0.1 33.6
34.7	1.0	32.3	<0.1 32.3
30.7	1.0	28.6	<0.1 28.6
33.0	1.0	26.4	<0.1 26.4
28.4	1.0	19.0	0.1 19.0
22.1	1.0	18.8	0.1 18.8
20.8	1.0	14.6	0.1 14.6

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FIG. 3B-2

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Clone	Parental/Design	Sequence	Ratios over Background		Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
D820-3-H2-IR		<u>WLDQEWANVQCEVYGRGCPS</u>	44.8	1.4	24.2	0.1 17.2
D820-3-H2-IR		<u>RLDLEWANIQCEVYGRGCPS</u>	23.9	1.0	40.0	<0.1 40.0
D820-3-C4-IR		<u>WLEQEWARVQCEVYGRGCSS</u>	31.0	1.0	39.5	<0.1 39.5
D820-3-C3-IR		<u>WLEQEWILVECEVYGRGCPT</u>	35.2	1.0	39.4	<0.1 39.4
D820-3-G6-IR		<u>WLEQEWAVQCEVWGRGCPS</u>	33.8	1.0	38.8	<0.1 38.8
D820-3-D2-IR		<u>WLDQEWEWIQCEVYGRGCPL</u>	35.6	1.0	37.8	<0.1 37.8
D820-3-D3-IR		<u>LLDEEWAQIECEIYGRGCPS</u>	34.8	1.0	37.7	<0.1 37.7
D820-3-B5-IR		<u>ALDEEWANVQCEVYGRGCHF</u>	34.1	1.0	37.1	<0.1 37.1
D820-3-E2-IR		<u>C?EQEWGLVQCEVYGRGCPS</u>	34.4	1.0	37.0	<0.1 37.0
D820-3-B3-IR		<u>WLEQEWAYVQCEVYGRGCPS</u>	33.6	1.0	36.7	<0.1 36.7
D820-3-B6-IR		<u>WLEHEWAQVQCEVWGRGCPY</u>	31.2	1.0	36.6	<0.1 36.6
D820-3-D4-IR		<u>WLEQEWAEVRCEVYGRGCPR</u>	32.0	1.0	36.2	<0.1 36.2
D820-3-C2-IR		<u>?LEQEWANVQCEVYGRGCPS</u>	33.7	1.0	35.6	<0.1 35.6
D820-3-F6-IR		<u>WLEQEWAGIQCKVYGRGCPS</u>	30.8	1.0	35.2	<0.1 35.2
D820-3-D5-IR		<u>RLEQEWAVQCEVWGRGCLP</u>	30.5	1.0	34.8	<0.1 34.8
D820-3-F5-IR		<u>QLDHEWAGIQCEVWGRGCPS</u>	29.8	1.0	34.6	<0.1 34.6
D820-3-H3-IR		<u>WLEQEWAGIQCEVYGAGCRS</u>	30.2	1.0	33.8	<0.1 33.8
D820-3-G2-IR		<u>SLEQEWANVQCVYGRGCPI</u>	31.3	1.0	33.0	<0.1 33.0
D820-3-H6-IR		<u>WLEQEWADQVLCVYGRGCPY</u>	30.3	1.0	32.2	<0.1 32.2
D820-3-F3-IR		<u>WLEQEWAV?CEVYGRGCA?</u>	28.6	1.0	30.7	<0.1 30.7
D820-3-B4-IR		<u>WMDQEWANVQCEVYGRGCPS</u>	33.1	1.0	30.5	<0.1 30.5
D820-3-C5-IR		<u>QLDQEWANVQCEVYGRNCRT</u>	29.1	1.0	30.3	<0.1 30.3
D820-3-F4-IR		<u>TLEQEWAVICEVYGRGCLS</u>	25.9	1.0	29.5	<0.1 29.5
D820-3-H5-IR		<u>RLEQEWAVQCEVWGRGCLS</u>	26.3	1.0	28.6	<0.1 28.6
D820-3-A6-IR		<u>WLDQEWALVQCEVYGRGCPA</u>	24.8	1.0	26.0	<0.1 26.0
D820-3-A2-IR		<u>WLDQEWAGIQCHVWGRGCPA</u>	23.7	1.0	25.6	<0.1 25.6
D820-3-G5-IR		<u>WLEQEWANVQCEVYGRGCPS</u>	22.6	1.0	25.0	<0.1 25.0
D820-3-G3-IR		<u>RLEEEWANVQCVYGRGCPS</u>	22.2	1.0	23.9	<0.1 23.9
D820-3-E3-IR		<u>WLEQEWVRIQCEVYGRGCPS</u>	20.6	1.0	22.7	<0.1 22.7

FIG. 3C-1

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Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGF3R	IR	IGFR/IR IR/IGFR
D820-3-E5-IR	WLDQEWAWVQCEVYGRGCPS	44.8	1.4	24.2	0.1 17.2
D820-3-D1-IR	WLEQEWTVVQCEVYGGCPS	25.9	1.0	22.6	<0.1 22.6
D820-3-E1-IR	WLEKEWAGVQCEIYGRGCPS	27.3	1.0	22.4	<0.1 22.4
D820-3-F1-IR	WLEEWAWVRCEVYGRGCQS	22.4	1.0	21.9	<0.1 21.9
D820-3-B2-IR	WLEHEWAIQCELYGRGCTY	22.0	1.0	21.0	<0.1 21.0
D820-3-A3-IR	ALEEAWAWVQCEVYGRGCPS	13.1	1.0	18.4	0.1 18.4
D820-3-H4-IR	WLEQEWAVQCEVYGRGCPS	23.5	1.0	18.4	0.1 18.4
D820-3-G1-IR	WLDDAWAIQCEIYGRGCQS	25.6	1.0	17.5	0.1 17.5
D820-3-C1-IR	QLEEWAGVQCEVYGRGCPS	14.5	1.0	16.3	0.1 16.3
D820-3-A1-IR	WLEQEWLLVQCGVYGRGCPS	27.8	1.0	13.9	0.1 13.9
D820-3-A5-IR	WLDQEWAWIQCEVYGRGCRS	14.7	1.0	12.8	0.1 12.8
D820-3-H1-IR	WLEQEWAVQCEVSGRGCP	6.4	1.0	6.3	0.2 6.3
D820-3-A4-IR	W?DQEWALIQCEVYGRGCPS	13.7	1.0	6.2	0.2 6.2
D820-4-E12-IR	SLDEEWAGVLCVYGRGCPS	6.0	1.0	4.3	0.2 4.3
D820-4-B12-IR	SVDQELEWLMCHFQGRVCP	34.9	9.0	10.9	0.8 1.2
	WLEQERAWIWCIEIQSGCRA	32.2	8.6	1.0	8.6 0.1

FIG. 3C-2

Clone	Parental/Design	Sequence	Ratios over Background			Comparisons	
			E-Tag	IGFsR	IR	IGFR/IR	IR/IGFR
D820-3-D5-IGFR		WLDQEWAWVQCEVYGRGCPS	44.8	1.4	24.2	0.1	17.3
D820-3-E4-IGFR		WVNQALGGVQSDVQGRRCQS	29.6	3.8	1.0	3.8	0.3
D820-3-C5-IGFR		LLDHEWPWVGCEVCGRGSLS	27.1	3.2	1.0	3.2	0.3
D820-3-F4-IGFR		WLHQELAWVRGEGYPRRRS	25.0	3.1	1.0	3.1	0.3
D820-3-F6-IGFR		WLGHDWAWIQCEVYGLGPC	3.9	2.7	1.0	2.7	0.4
D820-3-G4-IGFR		WIDQEGVRVQCEA*GRAFPS	26.7	2.6	1.0	2.6	0.4
D820-3-E2-IGFR		WRDEEAWVQGVVQGRGWA	3.8	2.6	1.0	2.6	0.4
D820-3-G6-IGFR		RLGVESWFORKVYGRDSTS	15.3	2.6	1.0	2.6	0.4
D820-4-E11-IGFR		WLAQGWAGVQCVVYGRGCRN	20.3	2.4	1.0	2.4	0.4
D820-4-H11-IGFR		WLEEE*AGIQCV?GRGCPS	12.6	1.0	3.0	0.3	3.0
D820-4-D11-IGFR		WLDQEWVQCEVWGRGCLS	8.1	1.0	4.6	0.2	4.6
D820-4-A8-IGFR		RLEQEWALIQCEVYGRGCPS	4.5	1.0	5.3	0.2	5.3
D820-4-F9-IGFR		WLEEEWAQVQCVVYGRGCAS	3.2	1.0	5.5	0.2	5.5
D820-4-C8-IGFR		WLDLE*EWLQCEVYGRGCAT	9.4	1.0	5.8	0.2	5.8
D820-4-D9-IGFR		WLEQEWVQVRCVYGRGCPS	11.6	1.0	5.9	0.2	5.9
D820-4-D7-IGFR		WLEEEWAQVQCEVYGRGCPS	10.1	1.0	8.9	0.1	8.9
D820-4-H9-IGFR		WLDQEWARVQCEVWGRGCTY	34.1	3.5	33.4	0.1	9.5
D820-4-E10-IGFR		YLD?EAWVQCEVYGLGCQS	18.4	1.0	10.1	0.1	10.1
D820-4-E7-IGFR		WLDVE*AWVQCEVWGRGCPS	26.7	2.6	27.0	0.1	10.4
D820-4-H8-IGFR		WLEQEWER?QCEVYGRGCPP	31.9	3.0	32.2	0.1	10.7
D820-4-A11-IGFR		WLEEEWAQVQCEVYGRGCLS	16.1	1.0	11.7	0.1	11.7
D820-4-C9-IGFR		WLDQEWAWIQCEVYGRGCPS	8.0	1.0	12.5	0.1	12.5
D820-4-E9-IGFR		?LEHEWAQIQCEV?GRGCQS	19.6	1.0	14.9	0.1	14.9
D820-4-B10-IGFR		WL?QEWAWIQCEVYGRGCPF	19.3	1.0	17.3	0.1	17.3
D820-4-F10-IGFR		WLD?EAWVQCEVYGRGCPS	19.3	1.0	21.5	<0.1	21.5
D820-4-B9-IGFR		GLEQGCPPVGLVQCRGCPS	27.8	1.0	25.7	<0.1	25.7
D820-4-G8-IGFR		WLEEEWAQVQCEVYGHGCPS	31.7	1.0	26.5	<0.1	26.5
		WLDQEWAWIQCEVYGRGCSS	25.6	1.0	29.3	<0.1	29.3

FIG. 3D-1

Clone Parental/Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR
D820-4-G9-IGFR	<u>WLDQEWAWVQCEVYGRGCPS</u>	44.8	1.4	24.2	0.1	17.3
D820-4-C10-IGFR	<u>WLDQEWAVQCEVWGRGCPS</u>	36.8	1.0	29.6	<0.1	29.6
D820-4-A9-IGFR	WLDLEWEFVQCEVYGRGCPT	32.6	1.0	31.3	<0.1	31.3
D820-4-B8-IGFR	WLEQEWASVQCEVYGRGCPS	20.4	1.0	31.4	<0.1	31.4
D820-4-F8-IGFR	WLDLEWEQIKCKVYGRGCPF	31.1	1.0	32.7	<0.1	32.7
D820-4-H7-IGFR	WLEQEWAIQCIYGRGCPS	28.3	1.0	32.9	<0.1	32.9
D820-4-E8-IGFR	WLEQEWALVLCVYGHGCPA	34.1	1.0	32.9	<0.1	32.9
D820-4-G10-IGFR	WLEQEWAIQCEVWGRGCSS	26.6	1.0	33.2	<0.1	33.2
D820-4-D10-IGFR	WLE?EWEVQCEVYGRGC?S	37.5	1.0	33.2	<0.1	33.2
D820-4-D8-IGFR	WLEQEWAVQCDVYGRGCPS	36.6	1.0	33.5	<0.1	33.5
D820-4-A10-IGFR	WLEQE*ARVQCEVWGRGCPS	23.7	1.0	34.6	<0.1	34.6
D820-4-B7-IGFR	WL?QEWARVHCEVWGRP?QC	29.4	1.0	35.5	<0.1	35.5
D820-4-E12-IGFR	PLEHEWAVQCVYGRGCRS	35.4	1.0	36.9	<0.1	36.9
D820-4-H10-IGFR	SLE?EWAUVQCEV?GRGCP?	37.0	1.0	37.0	<0.1	37.0
D820-4-F12-IGFR	WLDQEWVRVQCEVWGRGCPS	36.8	1.0	37.1	<0.1	37.1
D820-4-F7-IGFR	SLDKEWAVKCEVYGRGCPS	36.9	1.0	37.3	<0.1	37.3
D820-4-G12-IGFR	LGDQEWAVWEV#GRGWPS	34.4	1.0	37.5	<0.1	37.5
D820-4-D12-IGFR	WLEEEWAIKCGVYGRGCPS	30.3	1.0	37.8	<0.1	37.8
D820-4-A12-IGFR	WLEEE*GWVQCEVWGRGCPP	37.2	1.0	38.6	<0.1	38.6
D820-4-C12-IGFR	CLDQEWAVQCPVYGRGCPS	30.4	1.0	39.3	<0.1	39.3
D820-4-A7-IGFR	QLELEWAVQCEVWDRGCPS	37.1	1.0	39.6	<0.1	39.6
D820-4-B12-IGFR	RLEQEWAWIQCEVYGRGCRF	35.4	1.0	40.8	<0.1	40.8
	SLEHE*AWVQCKVYGRGC?S	36.2	1.0	41.4	<0.1	41.4

FIG. 3D-2

Clone Parental/Design	Sequence	Ratios over Background			Comparisons	
		E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR
B6-4-G12-IR	<u>WLDQEWAWVQCEVYGRGCPS</u>	44.8	1.4	24.2	<0.1	17.3
B6-3-A11-IR	WLDQEWAWIQCEVYGRGCPP	4.4	1.0	6.9	0.1	7.1
	WLDQEWAVRCEVYGRGCPS	7.3	1.0	6.3	0.2	6.3

FIG. 3E

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
R20-4-C10-IGFR	XXXXXXXXXXXXXXXXXXXXXXXXXXXX PKGTRFRGDVDVWDGYSWLA	--	--	--	--
		37.8	3.8	--	--

FIG. 4A-1

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20F-4-B7-IGFR	XXXXXXXXXXXXXXXXXXXXXXXXXXXX TPIPAGGINIASWGGYTWLS	10.9	3.7	--	--
20F-4-E4-IGFR	HRGTVTGVVVARWPGYEWLS	8.9	4.7	7.3	0.1
20F-4-E12-IGFR	SDVWAQPORRNDWPGYHWLS	9.7	4.7	6.3	0.2
20F-4-F4-IGFR	HRGTVTGVVVARWPGYEWLS	13.9	10.1	6.0	0.2
20F-4-F7-IGFR	SDVWAQPORRNDWPGYHWLS	13.7	3.9	5.6	0.2
20F-4-E7-IGFR	RPHRINPQDDAVWPGYLWL	7.2	2.5	5.1	0.2
20F-4-F11-IGFR	HRGTVTGVVVARWPGYEWLS	17.6	16.2	4.7	0.2
20F-4-D10-IGFR	FGRGYGGDGGYWSGYEWLA	9.8	2.4	4.6	0.2
20F-4-B3-IGFR	DGLVVKSGREWPGYGLER.A	17.3	14.4	4.1	0.2
20F-4-B12-IGFR	DGSIV.VSSSVGWPGYEWLM	10.1	9.9	4.0	0.2
20F-3-A9-IGFR	WQANLSNGGGRWGGYDWLM	6.6	2.7	4.0	0.2
20F-4-G2-IGFR	FGRGYGGDGGYWSGYEWLA	5.1	1.3	4.0	0.2
20F-4-D11-IGFR	VNYEMDRVPPMPWGGYHWLS	5.0	1.0	2.7	0.4
20F-4-G4-IGFR	MGGGLWVGVIWPGYWSLSQ	3.9	0.9	2.3	0.4
20F-4-G12-IGFR	SDVWAQPORRNDWPGYHWLS	3.2	0.9	1.8	0.6
				1.5	0.7

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FIG. 4A-2

Clone Design	Sequence
R20 β -4-A4-IR	XXXXXXXXXXXXXXXXXXXXX
R20 β -4-F2-IR	WPGYLFFEEALQDWRGSTD
R20 β -4-E8-IR	SMFVAGSDRWPGYGVLDWL
	VRGFQGGTVWPGEWLRNAA

FIG. 4B-1

Ratios over Background		Comparisons	
E-Tag	IGF ₃ R	IR	IGFR/IR IR/IGFR
--	--	--	--
11.9	17.5	1.4	12.5 0.1
16.4	13.9	3.1	4.5 0.2
41.0	34.9	3.6	9.7 0.1

Clone Design	Sequence
20F-4-H10-IR	XXXXXXXXXXXXXXXXXXXXX
20F-4-C10-IR	LDLASGDSWLGYDVLRGWLS
	IHSSDGIGAGGGAWFRDVA

FIG. 4B-2

Ratios over Background		Comparisons	
E-Tag	IGF ₃ R	IR	IGFR/IR IR/IGFR
--	--	--	--
10.2	3.1	2.4	1.3 0.8
23.4	9.6	4.1	2.3 0.4

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Clone Design	Sequence
R20 β -4-D10-IR	XXXXXXXXXXXXXXXXXXXXX
R20 β -4-D9b-IR	LGPLLRWGSEVCGVWPDICE
R20 β -4-H4-IR	PFGFGGRWWGIPRMWWYRNS
R20 β -4-A2-IR	WWGGRNRWWLERWGLGGER
	GRVALWGPVWPRWWFMSRPV

FIG. 4C

Ratios over Background		Comparisons	
E-Tag	IGF ₃ R	IR	IGFR/IR IR/IGFR
--	--	--	--
21.5	1.0	8.0	0.1 8.0
32.6	6.8	15.1	0.5 2.2
11.6	1.7	3.6	0.5 2.1
17.1	2.6	5.2	0.5 2.0

Clone Design	Sequence	Ratios over Background			Comparisons		
		E-Tag	IGF _s R	IR	IGFR/IR	IR/IGFR	IR/IGFR
R40-3-40A2-IR	RGTRTDRLWKSGGFAIVPRWPCEFSYHCLVEWITKTGSPG	44.6	1.5	2.7	0.6	1.8	
R40-4-40F10-IR	GRTSMAFVPPRHRLQPELAPRPVRNHLVGGG	46.4	1.9	2.1	0.9	1.1	

FIG. 4D

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Clone Design	Sequence	Ratios over Background		Comparisons		
		E-Tag	IGF ₃ R	IR	IGFR/IR	IR/IGFR
	XXXXXXXXXXXXXXXXXXXXXXXXXXXX	--	--	--	--	--
R20-4-F10-IGFR	CLGAGSFRAGILCLGGLPVS	35.5	6.0	--	--	--
R20-4-F7-IGFR	GFWATACGGLQICEELGLKP	29.1	4.7	--	--	--
R20-4-H9-IGFR	DLFCAYMAQAALGLGQDLSCG	25.7	3.0	--	--	--
R20-3-A4-IGFR	RHLLLPQIWIAS*GGWGMG	15.6	2.7	--	--	--

FIG. 4E

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Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
20C-3-H3-IGFR	xxxxcxxxxxxxxxxxxxxxxxxxxxxxxxxxx	--	--	--	--
20C-3-F4-IGFR	DHRLCGTDEYLMQDLFVRGLCRLIW	28.5	26.6	1.0	<0.1
20C-4-C10-IGFR	GLLFCKQLFTLAGLQPEAGCVSSSR	34.4	27.5	1.2	<0.1
20C-3-G5-IGFR	IWIACLDELLRGQVWSSCRRAPIG	35.5	24.4	1.3	0.1
20C-3-A2-IGFR	DWLRCLGVILSGGLTELANTGCVQG	29.3	21.1	1.1	0.1
20C-3-B4-IGFR	WFSFCLGGLLQAQEWVWGRDVGCI	33.9	18.3	1.1	0.1
20C-3-C6-IGFR	GYSWLRDVLMEKQAKKREGSVGRQ	39.8	29.1	1.9	0.1
20C-3-E2-IGFR	FLTRLRLGLS*ERGEAGGPYAQA	34.8	20.9	1.4	0.1
20C-3-A3-IGFR	FSGFCMGLERLSQVSLGYCGAGGG	34.8	28.1	2.0	0.1
20C-3-B1-IGFR	ISFRCQLFVLAGMHPCPVDVGEGF	33.7	14.3	1.2	0.1
20C-3-F5-IGFR	NTPNCSQDWGQESGFALLALTCK	30.2	9.8	0.9	0.1
20C-4-A7-IGFR	LQGFCELLATVTGVTGLGCLDYQPI	35.5	31.9	3.9	0.1
20C-4-F8-IGFR	GSSICNLLARAQIVELALCEMGVQE	33.3	19.3	2.8	0.1
20C-4-G11-IGFR	LSFACLLSQLSGVVLDPCLLGED	30.5	27.7	5.3	0.2
20C-3-E1-IGFR	GEHFCQLMSLCGDDCGPVNCGGS	24.7	13.3	2.8	0.2
20C-3-B6-IGFR	GWFECLLASLVLPQGRSRASAVC	34.0	5.1	1.6	0.3
	YRQECACSVGAVGFLCGLACLARSG	37.3	32.8	13.7	0.4

FIG. 4F-1

Clone Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
40F-4-D1-IGFR	xxxxcxxxxxxxxxxxxxxxxxxxxxxxxxxxx	--	--	--	--
40F-4-B1-IGFR	LSCLAYSRHGIWRPSTDLGLRSVGECSVSTRWGYDWF	4.9	4.6	0.3	0.1
40F-4-D10-IGFR	GLDHSDAVGVLHGFAPWA.ARGWEAGGLEDTWAGYDWL	4.1	3.0	0.2	0.1
40F-3-A3-IGFR	W.GYAWLS	4.9	4.5	0.4	0.1
40F-4-C4-IGFR	LSCLAYSRHGIWRPSTDLGLRSVGECSVSTRWGYDWF	2.6	2.0	0.3	0.1
	EAMAVGLQCPARFVRAAAHGDGGSWGQDHF.AWGGYWWLG	3.8	2.0	4.1	0.2

FIG. 4F-2

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Clone Parental/Design	Ratios over Background		Comparisons	
	E-Tag	IGFsR	IR	IGFR/IR IR/IGFR
F815-4-G11-IGFR	39.1	1.8	27.7	0.1 15.4
F815-3-D1-IGFR	34.6	7.9	1.0	7.9 0.1
F815-4-C12-IGFR	14.9	1.0	2.0	0.5 2.0
F815-4-A11-IGFR	35.2	1.0	2.0	0.5 2.0
	5.4	1.0	2.1	0.5 2.1

FIG. 4G

Sequence
<u>HLSVLEELFWGASLFGYC</u> SG
HFYVLERLSGASLFGSGA
HREVERGLLWGAYQFCYCSG
FQSLLEELVWGAPLFRYGTG
HLSVLEELSWGASLFGQWAG

Clone Parental/Design
F815-4-G11-IGFR
F815-3-D1-IGFR
F815-4-C12-IGFR
F815-4-A11-IGFR

Ratios over Background	Comparisons	
	IGFR/IR	IR/IGFR
E-Tag	2.1	2.1
IGFsR	2.7	2.6
IR	2.6	2.5
IGFR/IR	6.7	2.3
IR/IGFR	9.5	2.0
IGFR/IR	2.3	1.8
IR/IGFR	2.3	1.7
IGFR/IR	2.1	1.7
IR/IGFR	3.2	1.6
IGFR/IR	6.9	1.5
IR/IGFR	3.9	1.3
IGFR/IR	2.9	1.3
IR/IGFR	1.7	1.2
IGFR/IR	1.5	1.2
IR/IGFR	1.6	1.1
IGFR/IR	1.5	1.1
IR/IGFR	2.9	1.0
IGFR/IR	1.4	1.0
IR/IGFR	7.0	0.9
IGFR/IR	8.6	0.8
IR/IGFR	6.0	0.8
IGFR/IR	2.7	0.7
IR/IGFR	8.2	0.6
IGFR/IR	5.3	0.1
IR/IGFR	0.7	

Ratios over Background

Comparisons

Sequence
HLSVLEELSWGASLFGQWAG
NLCRLEELAWGASLFGQCAG
APVSTEELRWGALLFGQWAG
HLSVLEERWWRESLFGQWAG
HLSVLEERWWRAALFGQWAG
HLSILEEQWWRESLFGQWAG
HMSVEELSWWASLFGKQAG
HLSLEERWWRATLFGQWAG
HLSVLEELWWRESLFGQWAG
HLSLLEEQWWRESLFGQWAG
HLSVLEERWWRETlFGQWAG
HLSVLEEQWWRESLFGQWAG
HLSVLEEQWW.ESLFGQWAG
HLSVLEELWWREALFGQWAG
HLSVLEERWWRATLFGQWAG
HL.VLEELLWGVSLFRQWAG
HLSALEEQWWRATLFGQWAG
HLSVLEERWWRATLLESQ
HLSALEELWWRETlFGQWAG
HLSVLEELWWRESLFGKQWAG
HLSVLEEAWWRESLFGHWAG
HMSEQEELWWRATLFGQWAG
HLSVLEERWWRETlFGQWAG
HRSVLKQLSWGASLFGQWAG

Clone Parental/Design
NNKH-4-A9-IR
NNKH-4-H4-IR
NNKH-4-B3-IR
NNKH-4-E1-IR
NNKH-4-E7-IR
NNKH-4-G3-IR
NNKH-4-B6-IR
NNKH-4-A10-IR
NNKH-4-A5-IR
NNKH-4-F11-IR
NNKH-4-C9-IR
NNKH-4-D12-IR
NNKH-4-D10-IR
NNKH-4-E5-IR
NNKH-2-A6-IR
NNKH-4-F6-IR
NNKH-4-C7-IR
NNKH-4-F7-IR
NNKH-4-F8-IR
NNKH-4-E9-IR
NNKH-4-E6-IR
NNKH-4-B7-IR
NNKH-2-B3-IR

FIG. 4H

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Clone Parental/Design	Sequence	Ratios over Background		Comparisons	
		E-Tag	IGFsR	IGFR/IR	IR/IGFR
NNKH-2-C5-IGFR	HL*VLEEL*LGASLFGQWAG	5.4	1.0	2.1	0.5
NNKH-2-D9-IGFR	HL*VLEEL*LGASLFGQWAG	7.3	0.9	0.7	1.3
NNKH-2-H12-IGFR	HL*VLEEL*LGASLFGQWAG	4.1	0.5	0.4	1.3
NNKH-2-D10-IGFR	HL*VLEEL*LGASLFGQWAG	5.0	1.3	1.1	1.2
NNKH-2-G9-IGFR	HL*VLEEL*LGASLFGQWAG	4.8	2.1	1.9	1.1
NNKH-2-C6-IGFR	HL*VLEEL*LGASLFGQWAG	1.9	1.4	1.3	1.1
NNKH-2-C7-IGFR	HL*VLEEL*LGASLFGQWAG	18.2	1.0	0.9	1.1
NNKH-2-F11-IGFR	HL*VLEEL*LGASLFGQWAG	21.8	1.3	1.3	1.0
NNKH-2-H3-IGFR	HL*VLEEL*LGASLFGQWAG	6.7	1.3	1.4	0.9
NNKH-2-B8-IGFR	HL*VLEEL*LGASLFGQWAG	4.7	0.7	0.8	0.9
NNKH-2-B12-IGFR	HL*VLEEL*LGASLFGQWAG	17.5	3.7	5.2	0.7
NNKH-2-F9-IGFR	HL*VLEEL*LGASLFGQWAG	1.2	1.0	2.9	0.3
	HL*VLEEL*LGASLFGQWAG	3.7	0.6	2.1	0.3

FIG. 4I

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D Name	Clonal Name	Formula #	K ₄ (μ M) HIR	PO 4	Fat Cell Assay	Activity	K ₄ (μ M) HGFR	Ratio IGF/IR	Sequence
D101	2003	1	0.51 0.27				13 11	25 41	KIGGGQHGDGNFYDWFVEALAKK (ϵ -biotin)
D102	2001	1	1.2 0.97				7.4 16	6.2 16	KVLQARHGCDSDCFYEWFAKK (ϵ -biotin)
D103	B8	1	0.74				15	20	KWSALLSVMDTGYAWFDDAVKK (ϵ -biotin)
D104	E7	1	20				>20	>1	KGSHWLVHRVDRFLFYEWFDLKK (ϵ -biotin)
D105	H8	1	2.8				12	4.3	KRDKPTDQEEQNWSFYEFWRHKK (ϵ -biotin)
D106	20F1	1	0.97				6.2	6.4	KVFWNCRSQOLDFYEWFEQAOKK (ϵ -biotin)
D107	40G11	1	1.1	YES		Antagonist	9.7	8.8	KLESHYWPQALDRFLFYSWFSKK (ϵ -biotin)
D108	3G11	1	2.3			Antagonist	19	8.3	KFYGWFSRQLSLIPRDDWGLPKK (ϵ -biotin)
D109	20H1	1	3.6			Antagonist	12	3.3	KSAPGLVSNKQDGLFYSWFREKK (ϵ -biotin)
D110	G3	1	0.84			Antagonist	1.4	1.7	KRGGGIFYEFESALRKHGAGKK (ϵ -biotin)
D111	D2	1	0.62				3.2	5.2	KOPERMQSDVGFYEFWFAVCGKK (ϵ -biotin)
D112	IGFR C1 A65-4-C1	1	0.49 0.19			Neutral	0.05* 0.02*	0.1 0.1	DYKDCWARPCGDAANFYDWFVQOASKK (ϵ -biotin)
D113	IGFR H2 A65-4-1+2	1	0.75		-20 μ M	Agonist	5.4	7.2	DYKDVFTTSVAFHENFYDWFVRQVSKK (ϵ -biotin)
D114	IGFR A6	1	8.1			Neutral	>20	>2.5	SAKNFYDWFVKK (ϵ -biotin)
D115	IGFR D5	1	8.1				>20	>2.5	ADKNFYDWFMAKK (ϵ -biotin)
D116	IGFR JBA5	9	4.4 cycli		>20 μ M	Agonist	8.1	1.8	DYKDLCSGWGRIGWLAGLCPKK (ϵ -biotin)
D117	IGFR H2C	1	0.70	YES	-20 μ M	Agonist	6.1 5.1	8.6 8.5	FHENFYDWFVRQVSKK (ϵ -biotin)
D118	20E2	2	0.25	YES	-20 μ M	Antagonist	1.3	5.2	DYKOFYDAIDQLVRC SARAGGTROKK (ϵ -biotin)
D119	20C11	2	0.25	YES	-20 μ M	Antagonist	13	2.9	KDRAFYNGLRDLVGAVYCAWDKK (ϵ -biotin)
D120	E8	10	0.37			Antagonist	2.5	0.8	KVRGFGGTWPGYEWLNRNAKK (ϵ -biotin)
D121	F2	10	1.1			Antagonist	2.2	5.9	KSMFVAGSDRWPGYGVADWLKK (ϵ -biotin)
D122	20A4 (A7)	6	1.2 1.0			Antagonist	7.4 >20 >20	6.7 >17 >20	KEIEAEWGRVRLVYGRGVGGKK (ϵ -biotin)
D123	D8	6	0.55 1.3			Antagonist	16 >20	29 >15	KWLDQEWAWQCEVYGRGCPSPKK (ϵ -biotin)
D124	F8	4	0.04* 0.09*				8.2 >20	200 >200	KHLVLEELFWGASLFGYCSGKK (ϵ -biotin)
D125	IGFR E4	1	2.6				>20	>8	DYKOERSAAGFRGNFYDWFVAQVKK (ϵ -biotin)
D126	IGFR D2C	1	1.4				18	13	LGENFYDWFVQVRKK

FIG. 5A

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Clonal Name	D or S name	Motif	Sequence	IR-Kd	IR-IC 50 Biacore	IR-IC 50 ^{FP} S175	P04	Fol Cell Assay
20-E2	D118	B6	DYKDFYDAIDQLVRGSGARAGGIROK K-biotin	250 nM		2.8 nM	+	++
C1	D112	A6	DYKDCWARPCCGDAANFYDWVQOAS KK-biotin	490 nM			-	0
D8	D123	C-C LOOP	KWLDQEWAWQCEVYGRGCSKK	550 nM			0	-
E8	D120	GROUP 6	KRGFGGTVWPGVWLRNA	370 nM			-	-
F8	D124	C-C LOOP	KHLCLLEELFWGASLFGYCSGKK	40 nM			-	0
H2C	D117	A6	FHENFYDWVROOVSKK	700 nM	>5 μM	5 nM	++	++
KCF9			RLYYEWFQGLEAQGRGGLS					
KC-G2		C-C-C	GLEGGCPWGLEVCRCGCPSS					
KCG7		B6	PYCGLEELSWGAALFGYCSG		>1 μM			
NG-C2		B6	GNQGMFYQLLSLLVGRDMH					
NG-G33		A6	GHSQCPESYDWVAGVSDPWVWCV					
NG-G8		B6	VEGRGLFYDLRLQARRQNG	2-4 μM	4.2 nM		+++	
NG-G9		B6	RAMSFYDALVGLGPKK-Biotin	>5 μM			-	
RP-1		A6	CSRPFHEQFYWFVDQLGL	1 μM			-	
RP-2		A6	RSEASFHVFYSWFEEQLRS	1 μM			+	
RP-3		A6	GRFYGWFDQADQLMPWGFQ	>10 μM			-	
RP-4		B6	PPWGARFYDAIEQLVFDNI	5 μM			+	
RP-5		B6	AGVNAFYRYFSILLQWVQGGK-Biotin	6 μM			-	
RP-6		B6+	TFYSCLASLLIGIPQPNRGPWERCCK-Biotin				+++++	
		C-C						
RP-7		A6	AAVHEQFYWFADQYKK					
RP-8		B6	QSFYDYTELLGGWKK		>5 μM		+	
RP-8#	S287	B6	QSFYDYTELLGGWEE					
RP-9		A6	GSIDESFYDWFERQLGKK			2.9 nM	++	
RP-10		B6	GSFYEALQRLVGGEQKK	>10 μM			+	
RP-11		A6	QAPSNFYDWVREWDKK	>10 μM			+	
RP-12		B6	DPFYQGLWEWLESGKK					
RP-13		A6	ASGFPENFYDWFGRLSLKK	>10 μM				
RP-14		A6	SACOFDCHENFYDWFAOKKK	>10 μM				
RP-15		A6	SQAGSAFYAWFDQVLRVKK					
RP-16		B6	VMDARDDPFYHKLSELVTKK					
RP-17		B6	QSDAFYSGIWLALGLSDGKK	>10 μM				
RP-18		B6	LQPCSGFYDFWQRLHLSGKK					
RP-19		A6	LKDGFDYDFWQRLHLSGKK					
RP-20		B6	GSASFYDAIDRLRMRIKK					
RP-24		GROUP 6	WPGYLFEEALQDWIRGSTED					
S167	S167	A6	AFYDWFAKK	>20 μM	No Binding			
S173	S173	R86	LDALDRLMRYFEERPSL	1.2 μM				
S174	S174	R86	PLAELWAYFEHSEQGRSSAH	16 μM				0
S175	S175	A6	GRVWLORNANFYDWFAVLG	230 nM	2-4 μM	0.9 nM	++	0
S176	S176	A6	NGVERAGIGDNFYDWFAVLH	470 nM				+++

FIG. 5B

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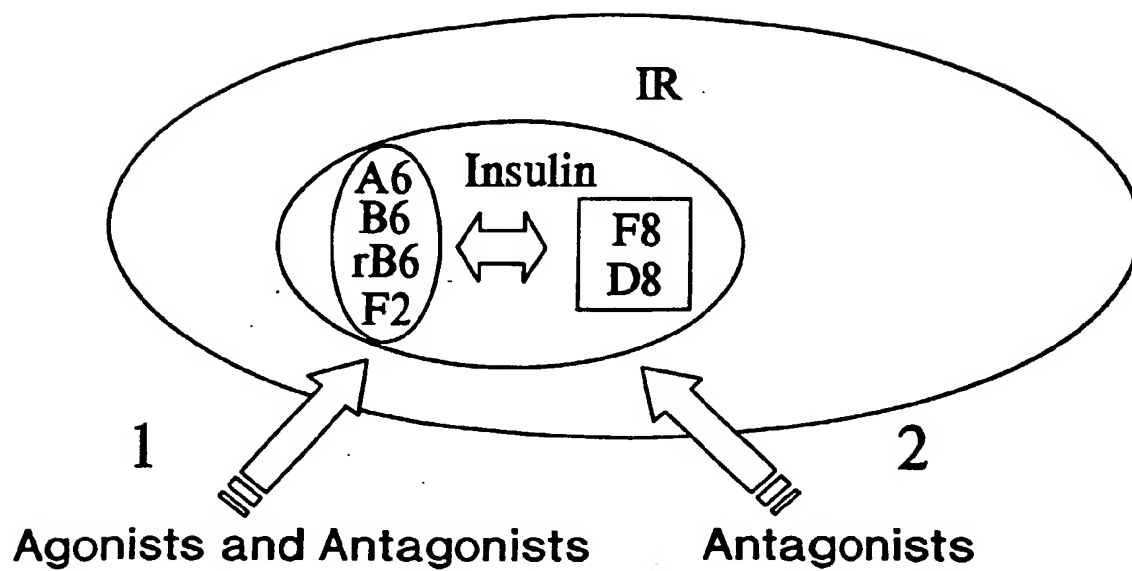


FIG. 6

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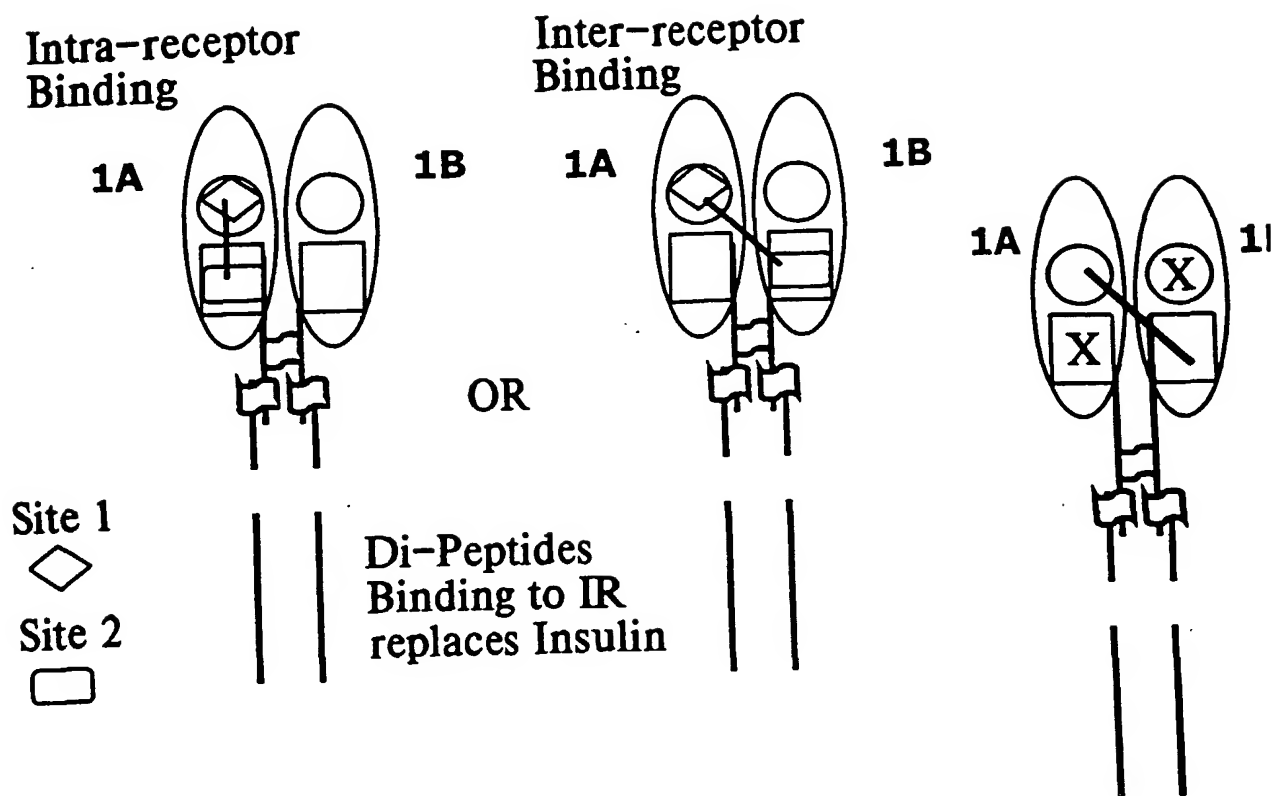


FIG. 7

Group 1 (Formula 1 Motif)		Target	
		Found	IR IGF
20D3*	IGGQGHQDGNFYDWFVEALA	18	+
20F1	VFNCRSQQLDFYEWFEQAA	16	+
G3	RGGGTFYEWFE ⁻ SALRKHGAG	8	+
20H1	RVAGAI ⁻ SAPGLVSNKQDGLFYSWFRE	5	+
20D1*	VLQARHGCD ⁻ SVSDCFYEWFA	4	+
D2	DPERMQSDVGFYEWFERAAVG	3	+
B8	WSALLSVMDTGFYAWFDDAV	2	++
C4	DIGSDGHGRRWDSFYRWFE ⁻ M	2	+
A8	IGGSFVEFYGWENDQV	2	+
E7	GHSWALVRHVDRLFYEWFDL	1	++
C8	LPAGGAQGF ⁻ AVRGFYEWFE ⁻ S	1	+
H8	RDKPTDQEEQNWSFYEWERH	1	+
E2	SRDQTNFTFNSAGFYGWFER	1	+
B12	GAFYRWFHEALVGSERVPDV	1	+
D10-2	RIGGGWARSEGEFYEWFEVREL	1	+
G8	RMFYEWFSQMGAGPTEGSA	1	+
H3	HEAFYDWF ⁻ SALVDGGYELMG	1	+
3G11	FYGWFSRQLSLTPRDDWG ⁻ L ⁻ P	1	+
F4	GVGTLTMSSDAFYTWFEV	1	+
E7-2	LGTSAGQGVGHRAFYQWFQ ⁻ S	1	+
40G11	<---ETLESHYVVPQ-----AALDRLFYSWF ⁻ S	3	+
40B2	IRDMHYVWQDRDRYINGVRQWYISDRYNPGSAFYRWFEID	2	+
40B12	RMGLQALAHYRKSA-----GPIFLSSGSVIKSEGDPFYAWFRLQ	1	+

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FIG. 8

Group 2: Formula 6 Motif		
Found	Target	
	IR	IGF
20A4*	+++	0
D8	+++	?

EIEAENGVRCLVYGRVCVG
WLDQEWAWVQCEVYGRGCPS

Group 3: Formula 2 Motif		
Found	Target	
	IR	IGF
20E2	+	++++
20C11	+	++++
20A12	+	++++
C6	+	++++
A6	+	++++
40H4	+	0

DYKDFYDAIDQLVRSARAGGTRD
DYKDDRAFYNGLRDLVGA VYGAWD
DYKDRLEFYCGIQALGANLGYSGCV
DYKDFYSALWGLCGVTGCC
RGQSDAFYSGI^{63/122}WALLIGLSDG
RYFPFGGFYGNLDVLRWLRPYVASPRWGHWRPGSLGKQPT

Group 5: Miscellaneous Motif 10		
Found	Target	
	IR	IGF
D9-2	++	++
H4	+	+

PFFGGRWWGI^{63/122}PRMWYRNS
WWWGGRNRWWLERWGLGGER

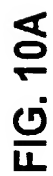
FIG. 9A

Group 4 and 6: Miscellaneous Motif 10			Target		
			Found	IR	IGF
D10	LGPLLRLWGSEVCGVWPDLC		3	++	0
A2	GRVALWGPVWPRWWFMSRPV		1	++	+
F2	SMFVAGSDDRWPYGVGLADWL		1	++	++
E8	VRGFQGGTVWPGYEWLRNAA		1	++	?
A4	WPGYLFFEEALQDWRGSTD		1	0	+++

Group 7: Formula 4 Motif			Target		
			Found	IR	IGF
B6	ACSSEFVKGPEGFLQCLGSI		1	0	++
F8	HLCVLEELFWGASLFGYCSG		4	+++	+
40D6	PERGRGLRTAMQLMRRPRDWHFPHSLEWGAPPLSG		1	0	0

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FIG. 9B



Displacement of ¹²⁵I-HI from HIR-11

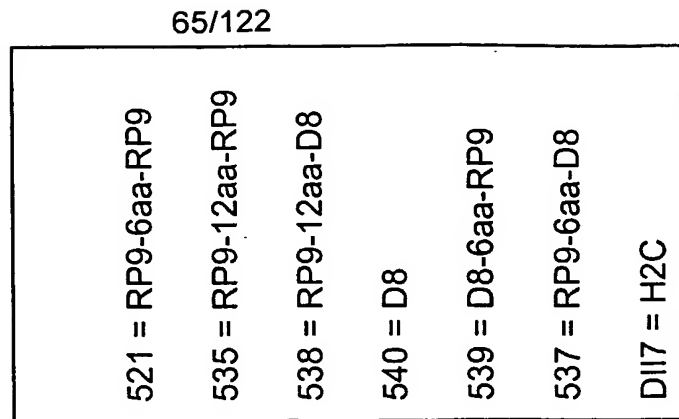
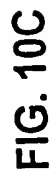
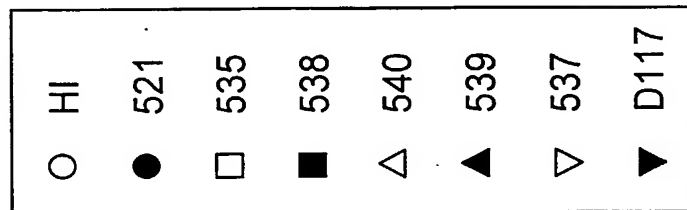
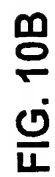
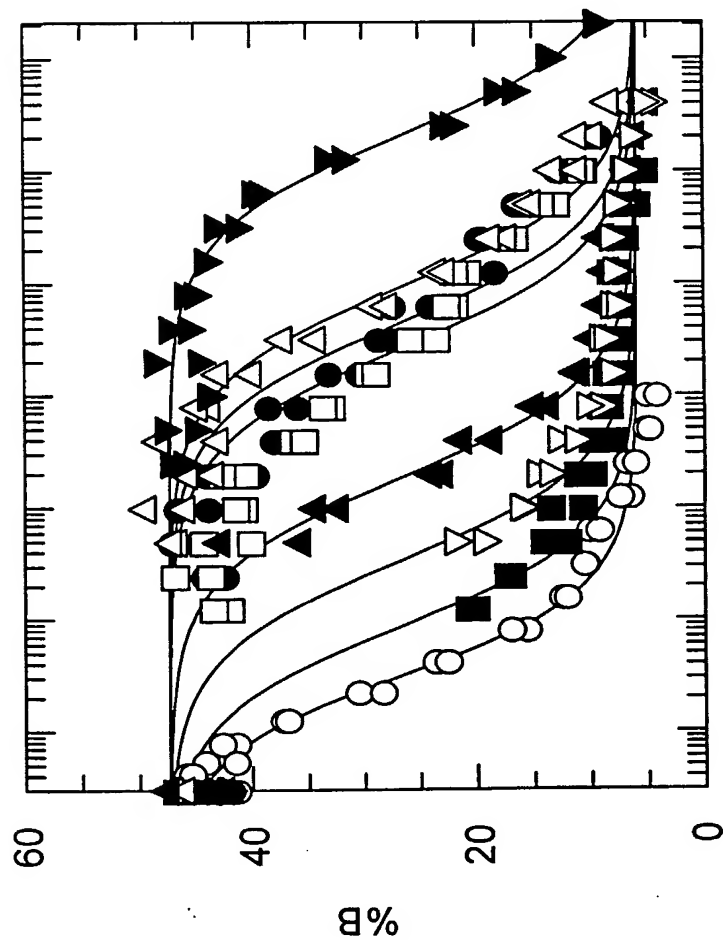


FIG. 11A

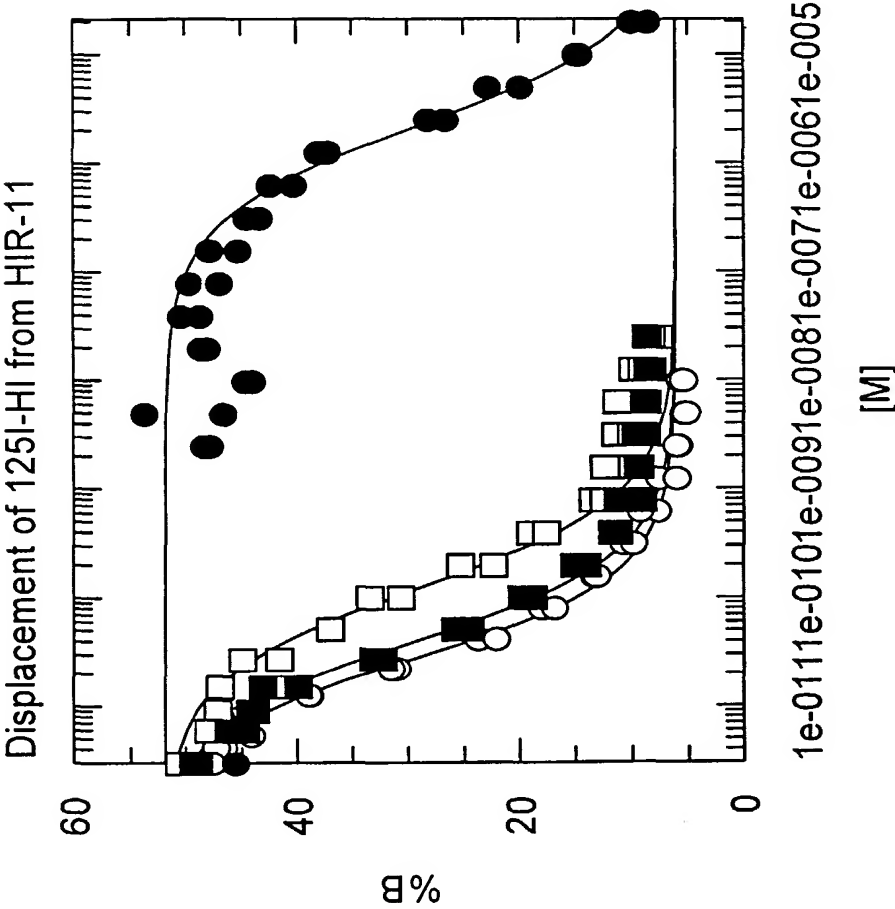


FIG. 11B

○	HI
●	D117
□	537
■	538

D117 = H2C
537 = RP9-6aa-D8
538 = RP9-12aa-D8

Kd	
HI	1.1e-11
D117	1.1e-6
537	5.9e-11
538	1.7e-11

FIG. 11D

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FIG. 12B

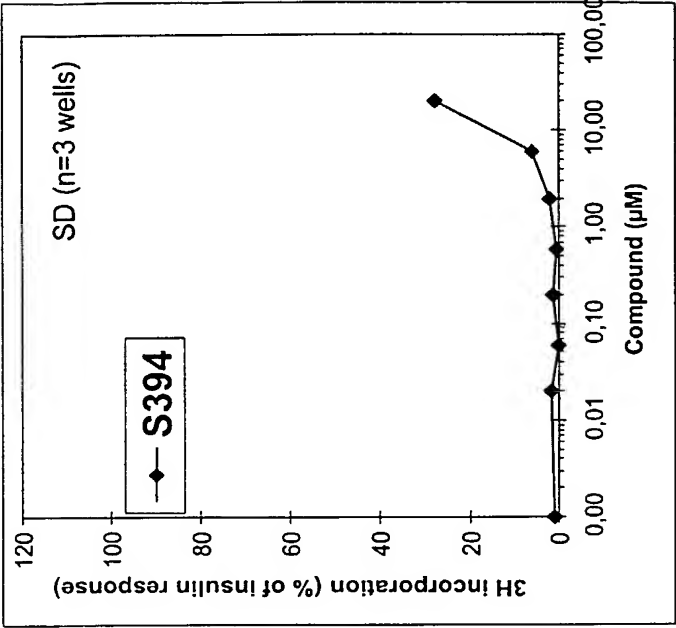
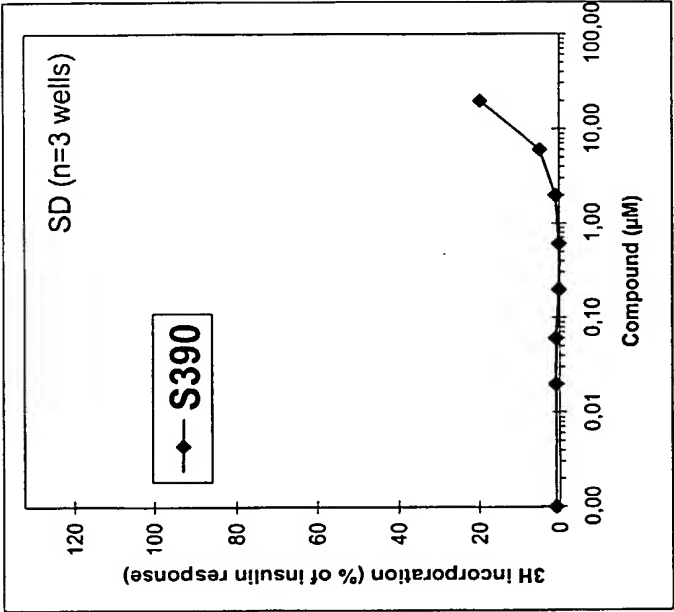


FIG. 12A



S390 = ESFYDWFERQLG
S394 = GSLDESFYDWFERQ

FIG. 12C

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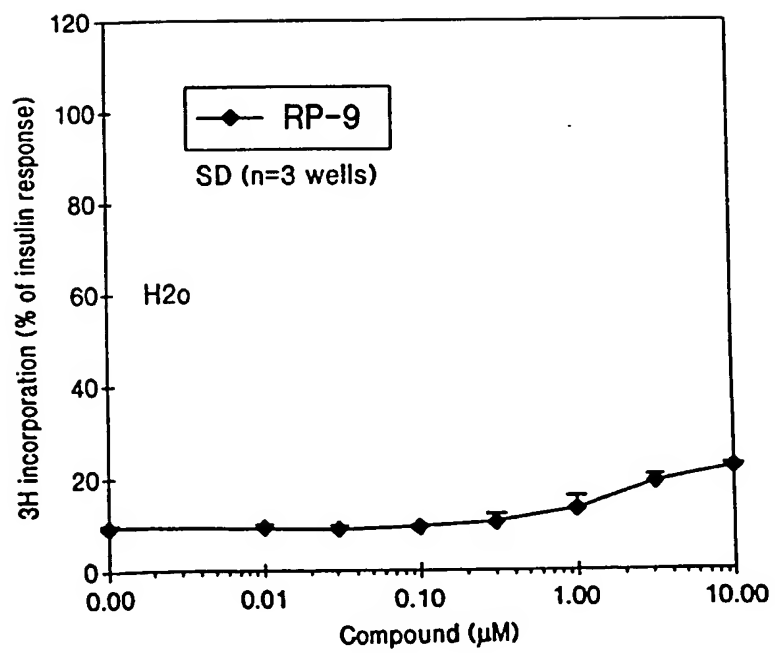


FIG. 12D

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FIG. 13B

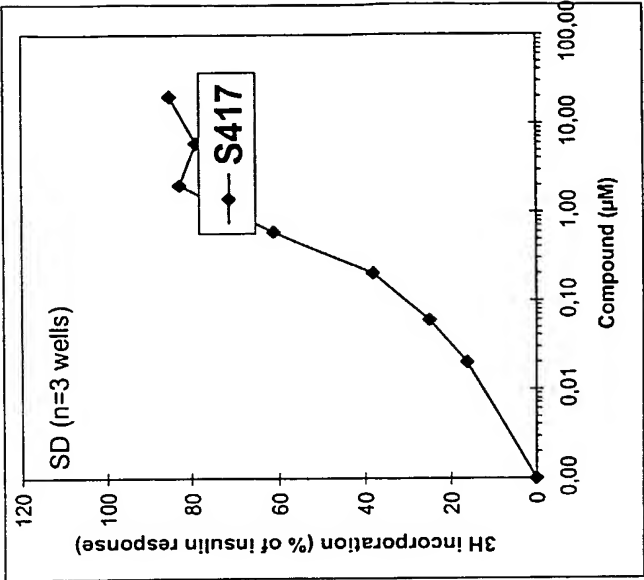
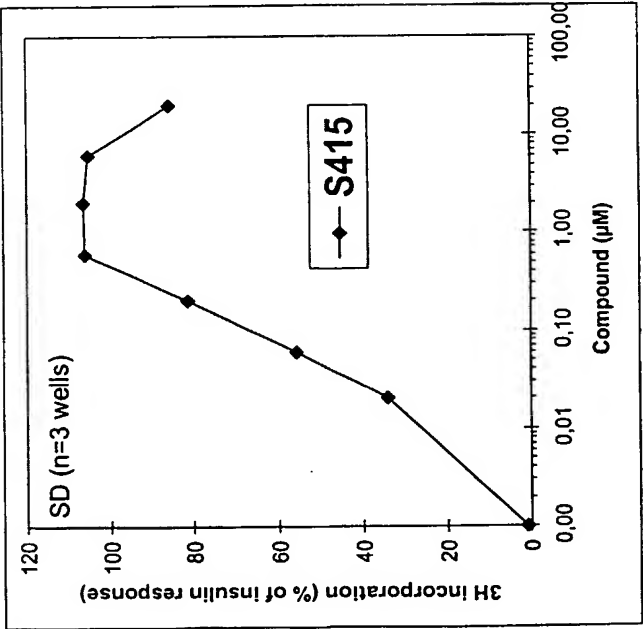


FIG. 13A



S415	(ESFYDWFERQLGK) ₂ -23
S417	23-(ESFYDWFERQLG) ₂

FIG. 13C

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FIG. 14B

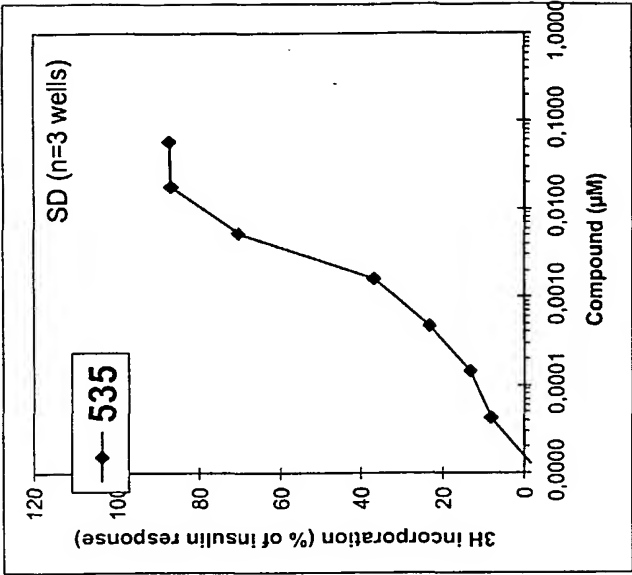
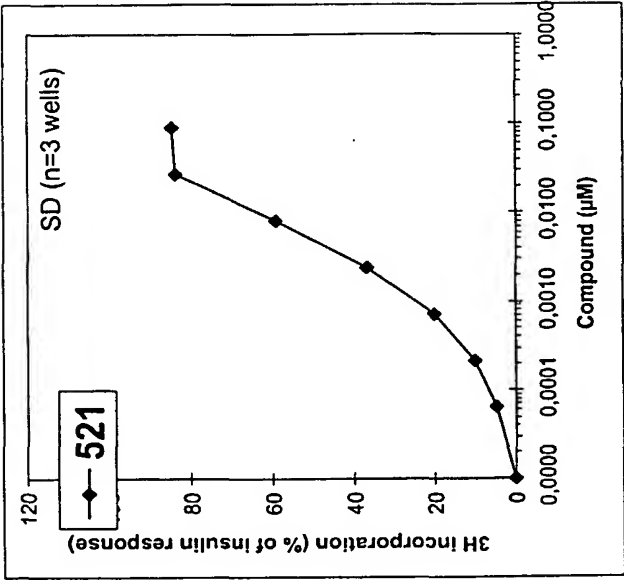


FIG. 14A



521 = RP9-6aa-RP9
535 = RP9-12aa-RP9

FIG. 14C

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FIG. 15B

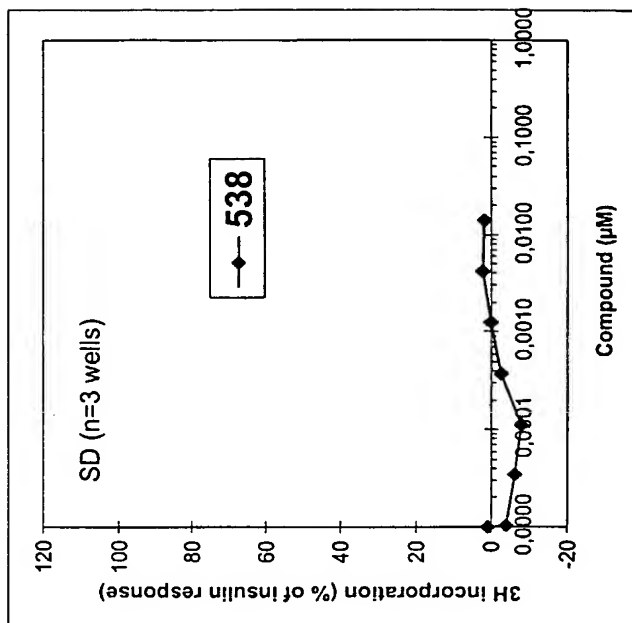
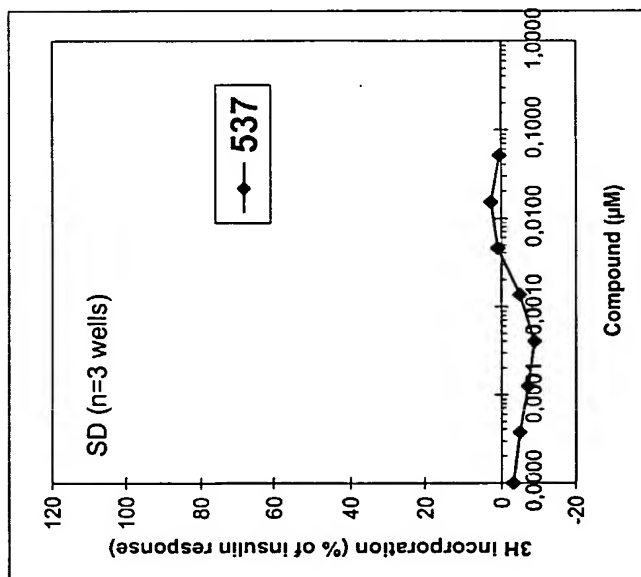


FIG. 15A



537 = RP9-6aa-D8
538 = RP9-12aa-D8

FIG. 15C

FIG. 16B

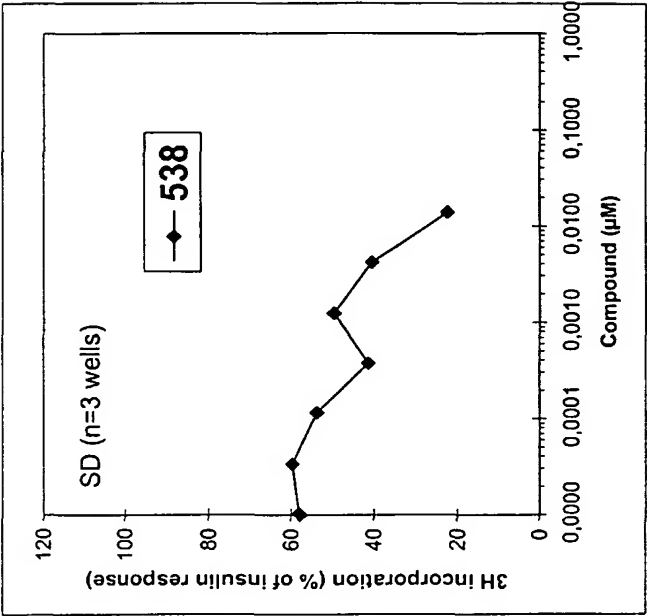
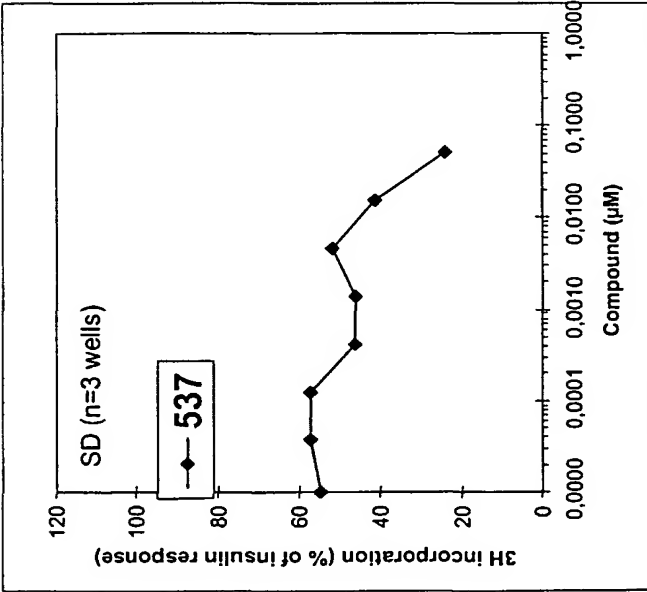


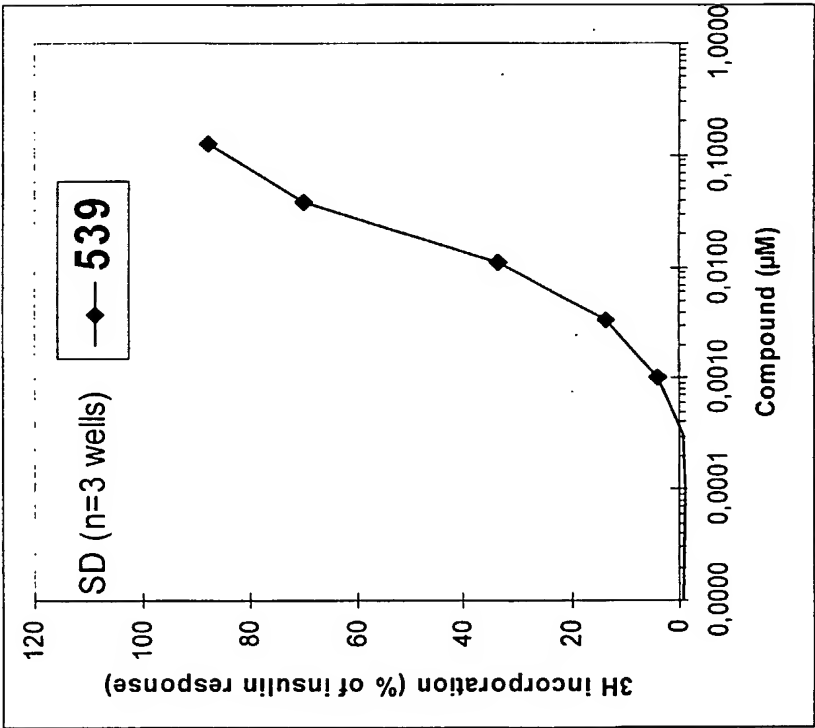
FIG. 16A



537 = RP9-6aa-D8
538 = RP9-12aa-D8

FIG. 16C

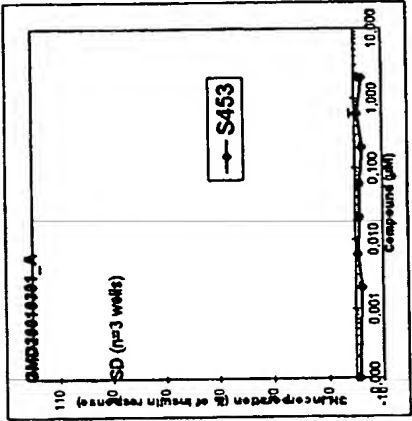
FIG. 17A



539 = D8-6aa-RP9

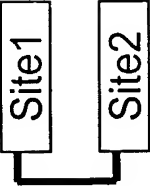
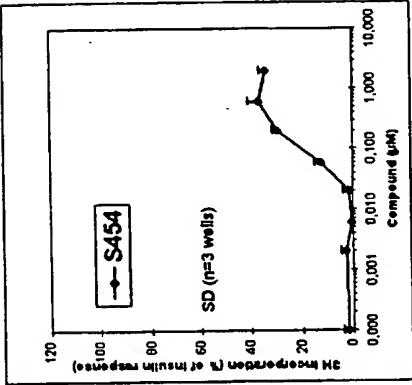
FIG. 17B

FIG. 18A



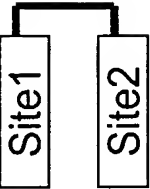
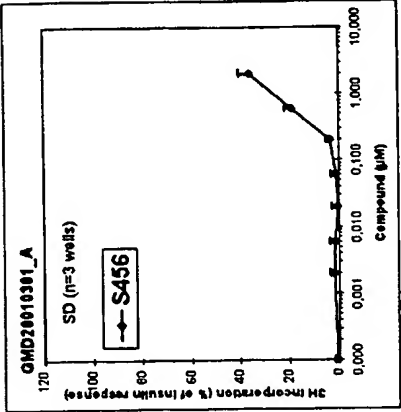
C-N

FIG. 18B



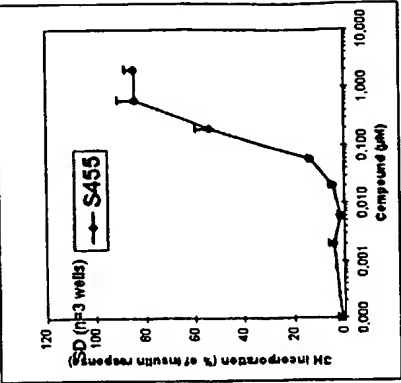
N-N

FIG. 18C



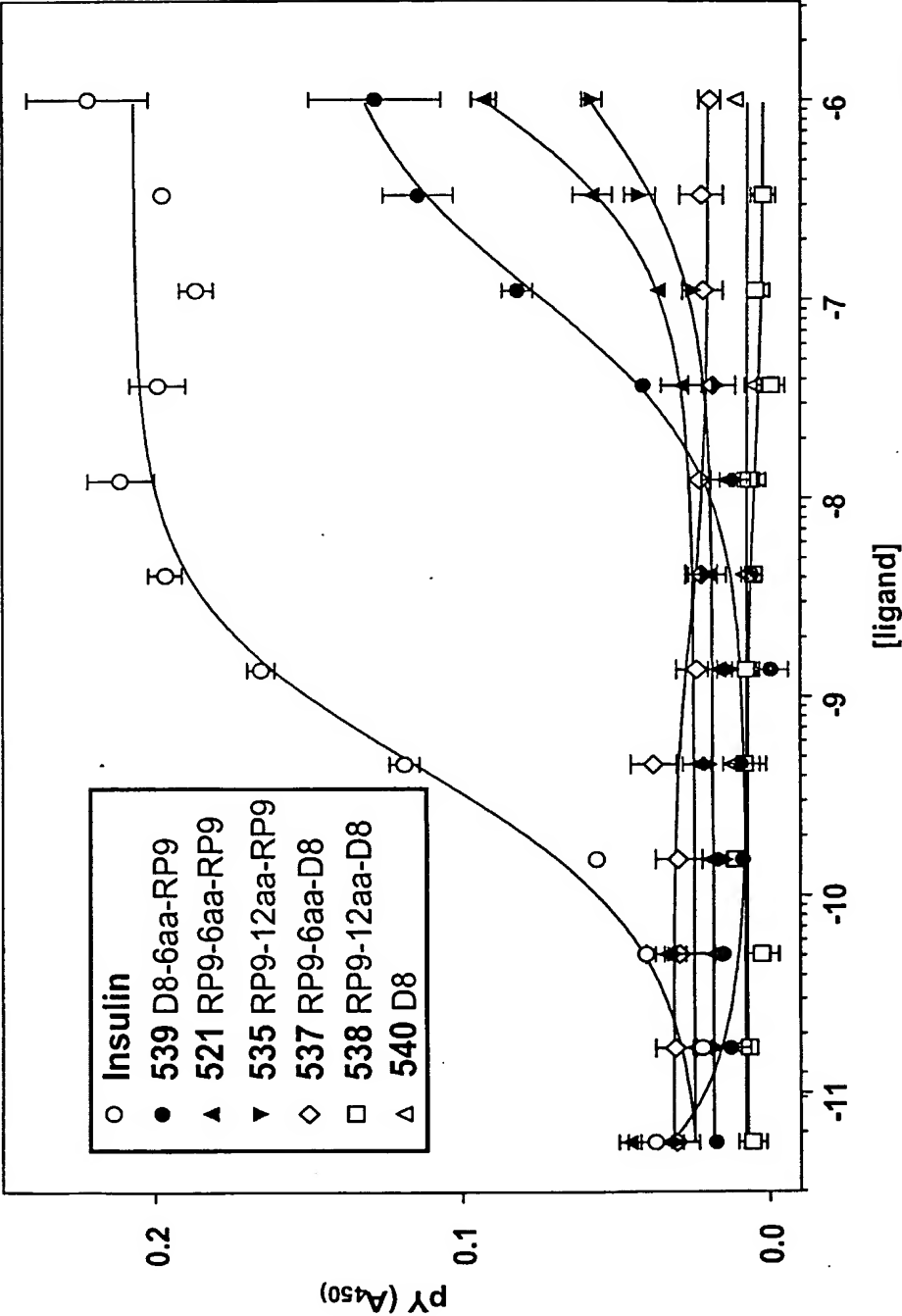
C-C

FIG. 18D



N-C

FIG. 19A

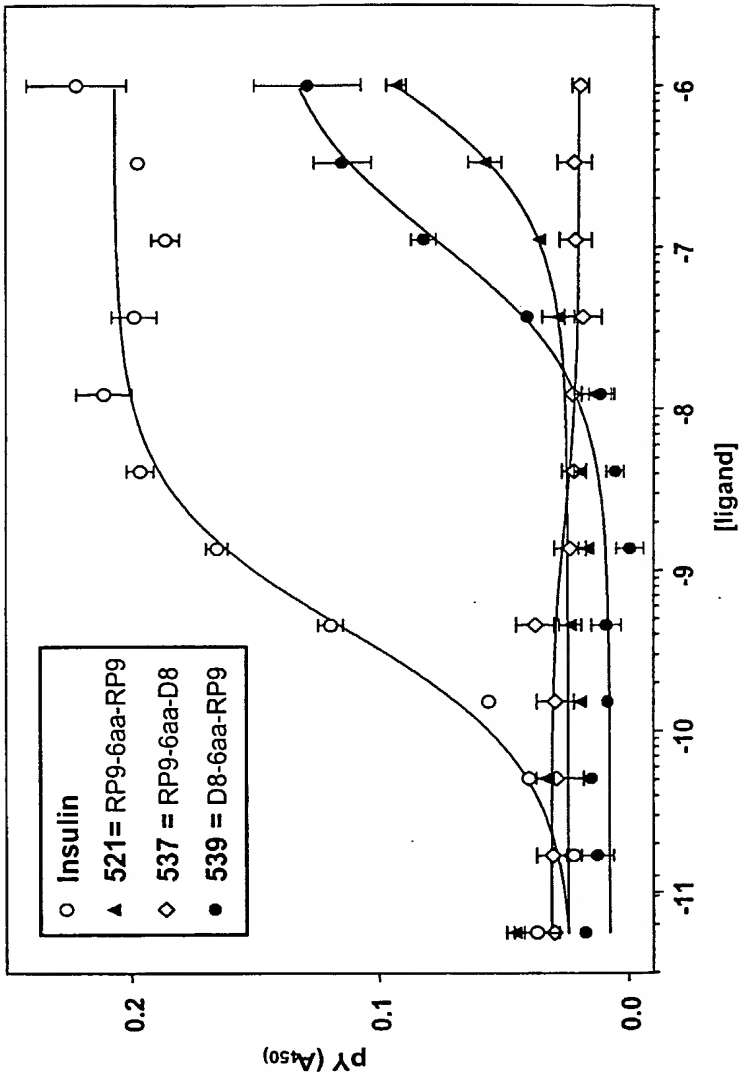


EC50	Insulin	521	535	539
	4.4680e-010	1.4420e-006	9.6490e-007	1.1000e-007

FIG. 19B

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FIG. 20A



	Insulin	521	539
EC50	4.4690e-010	1.4420e-006	1.1000e-007

FIG. 20B

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FIG. 21A

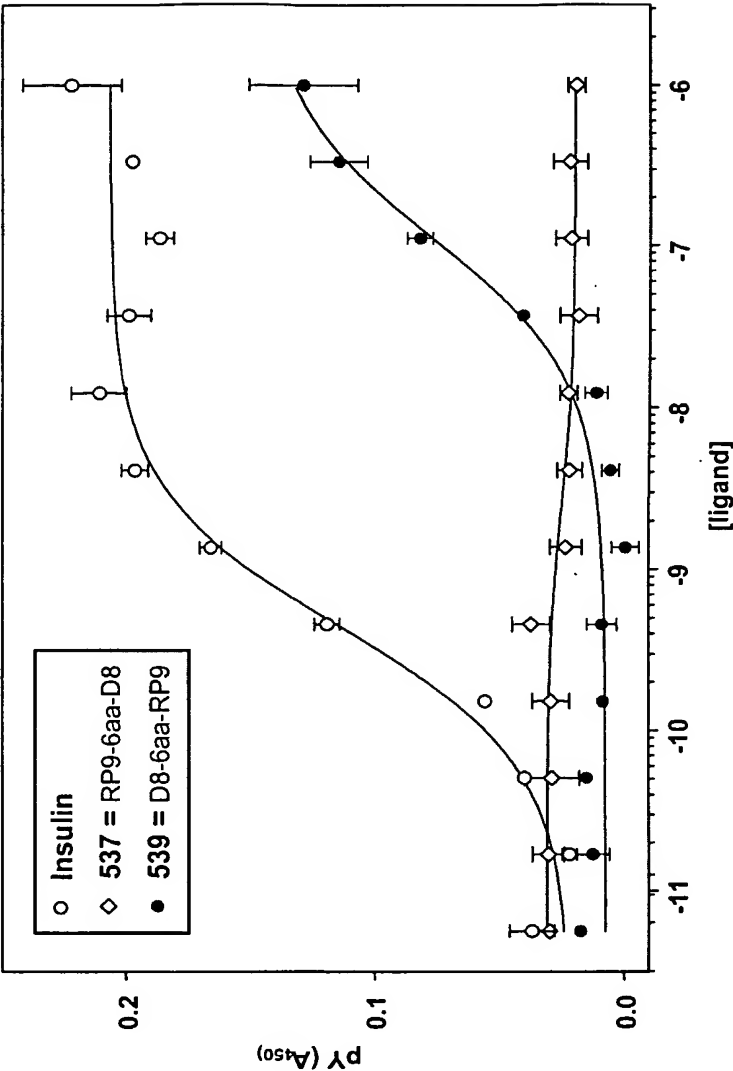
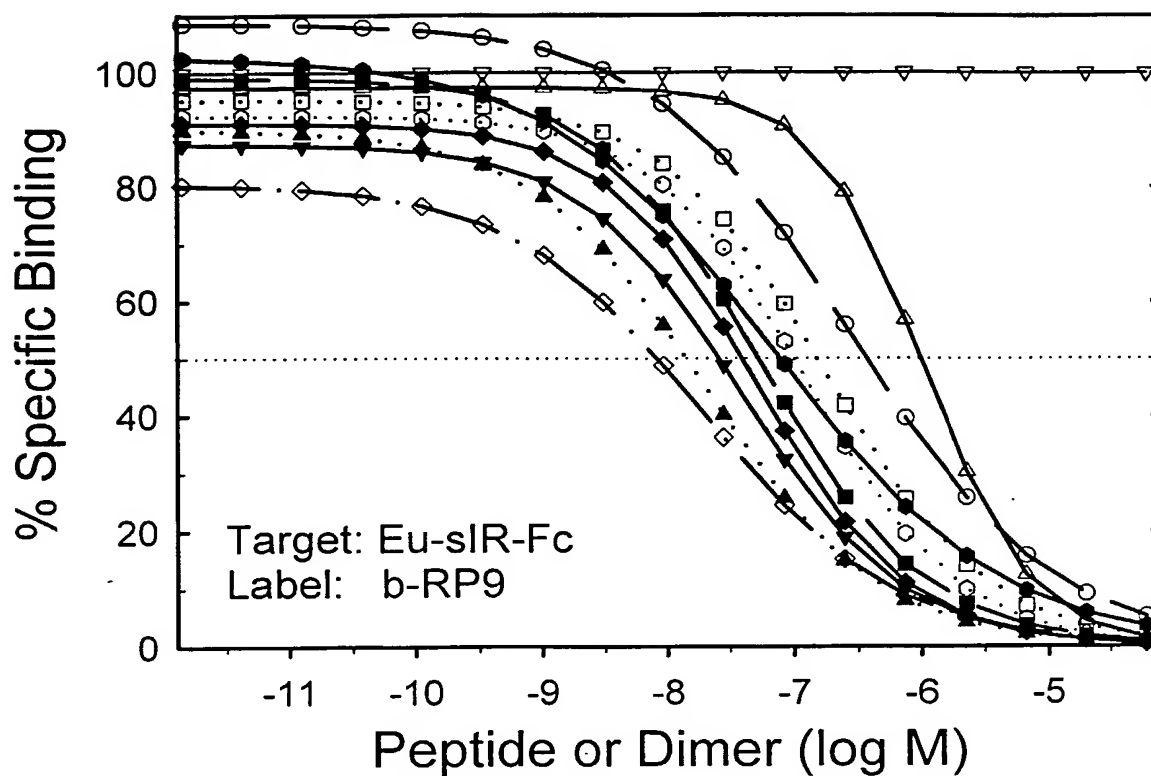


FIG. 21B

	Insulin	539
EC50	4.4680e-010	1.1000e-007

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FIG. 22A



Symbol	Peptide or Dimer	Sequence
△	H2C	FHENFYDWFVQRVSKK
□	S291	(Lig-GGG-H2C) ₂₋₉
▼	RP9	GSLDESFYDWFERQLGKK
■	S375	(RP9-Lig)- <u>14</u> -(RP9-Lig)
◇	S337	(RP9-Lig) ₂₋₂₃
○	S391	truncated(-GSLDE)RP9(-KK)
●	S390	truncated(-GSLD)RP9(-KK)
○	S414	(truncated(-GSLD)RP9(-KK)) ₂₋₁₄
◆	S175	GRVDWLQRNANFYDWFVAELG
▲	S380	(EE-short-S175-Lig) ₂₋₉
▽	Linker <u>23</u>	

FIG. 22B

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FIG. 23A

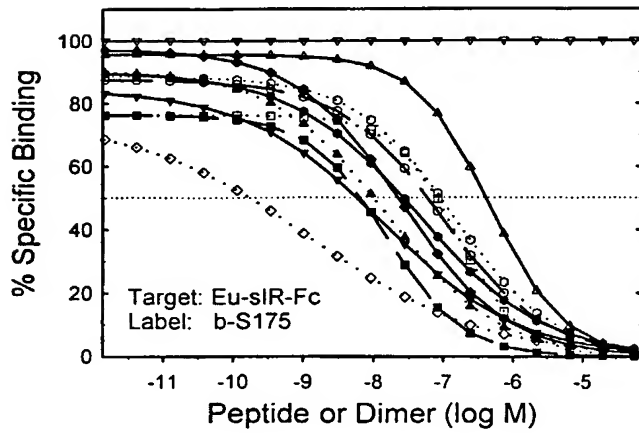
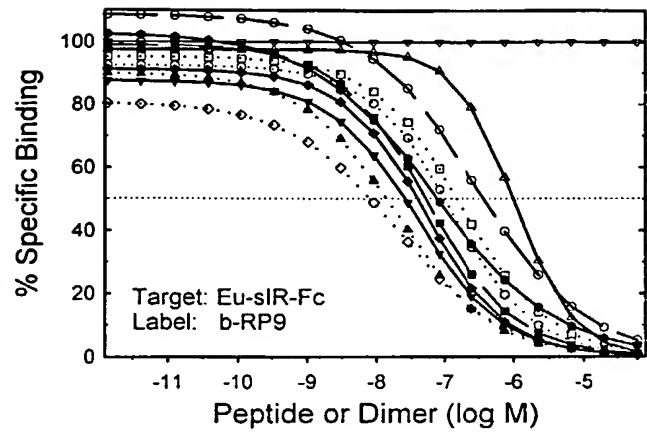


FIG. 23B

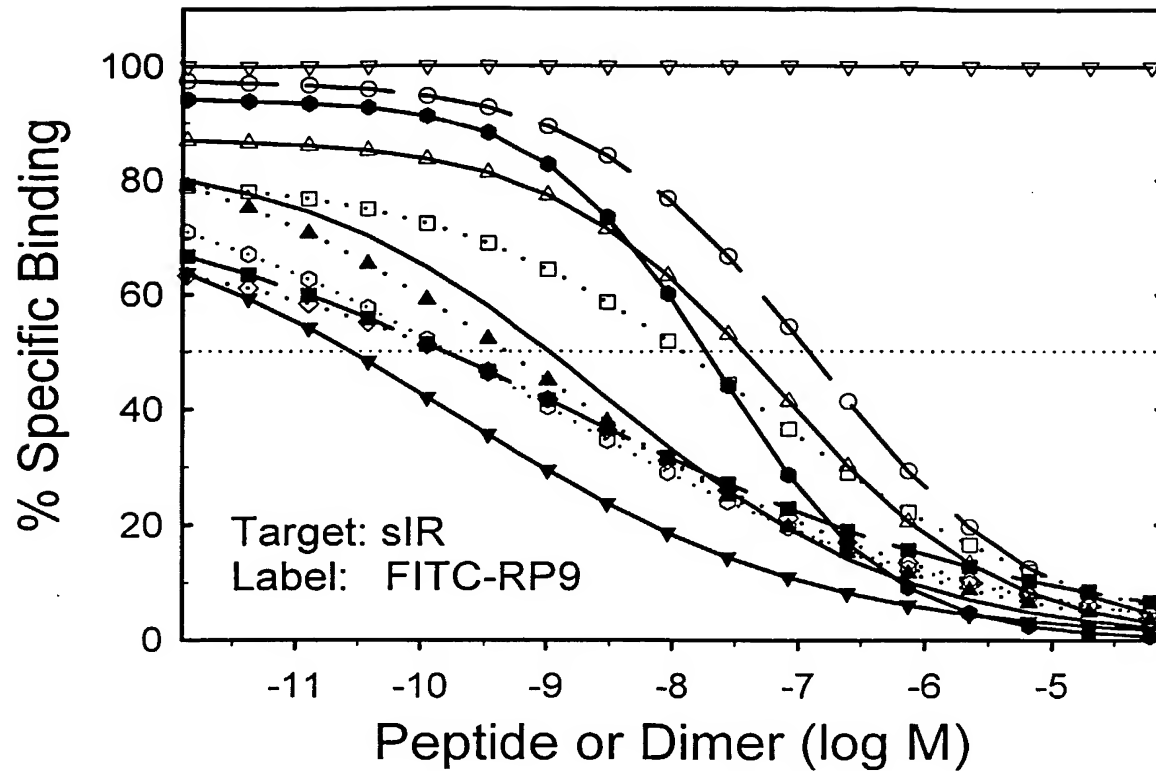


Symbol	Peptide or Dimer	Sequence
△	H2C	FHENFYDWFVQRVSKK
□	S291	(Lig-GGG-H2C) ₂₋₉
▼	RP9	GSLDESFYDWFERQLGKK
■	S375	(RP9-Lig) ₁₄ -(RP9-Lig)
◇	S337	(RP9-Lig) ₂₋₂₃
○	S391	truncated(-GSLDE)RP9(-KK)
●	S390	truncated(-GSLD)RP9(-KK)
○	S414	(truncated(-GSLD)RP9(-KK)) ₂₋₁₄
◆	S175	GRVDWLQRNANFYDWFVAELG
▲	S380	(EE-short-S175-Lig) ₂₋₉
▽	Linker <u>23</u>	

FIG. 23C

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FIG. 24A

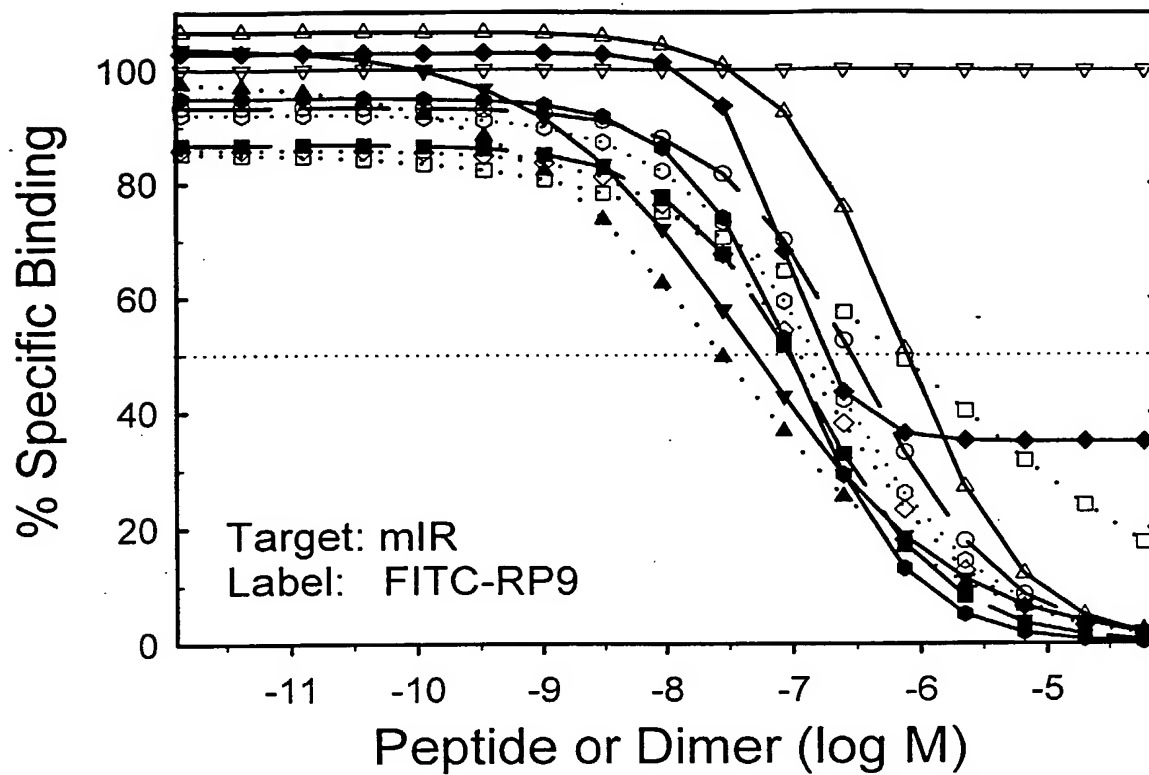


Symbol	Peptide or Dimer	Sequence
△	H2C	FHENFYDWVQRVSKK
□	S291	(Lig-GGG-H2C) ₂₋₉
▼	RP9	GSLDESFYDWFERQLGKK
■	S375	(RP9-Lig)- <u>14</u> -(RP9-Lig)
◇	S337	(RP9-Lig) ₂₋₂₃
○	S391	truncated(-GSLDE)RP9(-KK)
●	S390	truncated(-GSLD)RP9(-KK)
◊	S414	(truncated(-GSLD)RP9(-KK)) ₂₋₁₄
◆	S175	GRVDWLQRNANFYDWVFAELG
▲	S380	(EE-short-S175-Lig) ₂₋₉
▽	Linker <u>23</u>	

FIG. 24B

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FIG. 25A



Symbol	Peptide or Dimer	Sequence
△	H2C	FHENFYDWFVQRVSKK
□	S291	(Lig-GGG-H2C) ₂₋₉
▼	RP9	GSLDESFYDWFERQLGKK
■	S375	(RP9-Lig)- <u>14</u> -(RP9-Lig)
◇	S337	(RP9-Lig) ₂₋₂₃
○	S391	truncated(-GSLDE)RP9(-KK)
●	S390	truncated(-GSLD)RP9(-KK)
◊	S414	(truncated(-GSLD)RP9(-KK)) ₂₋₁₄
◆	S175	GRVDWLQRNANFYDWFVAELG
▲	S380	(EE-short-S175-Lig) ₂₋₉
▽	Linker <u>23</u>	

FIG. 25B

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FIG. 26A

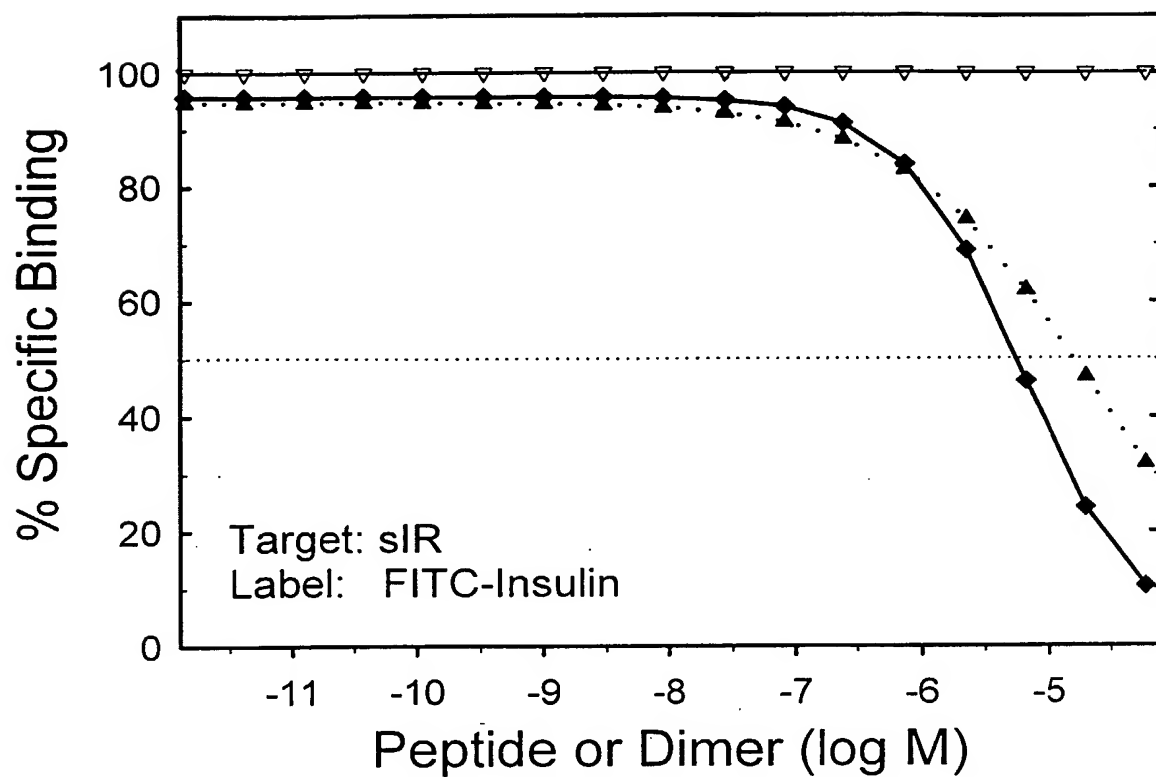
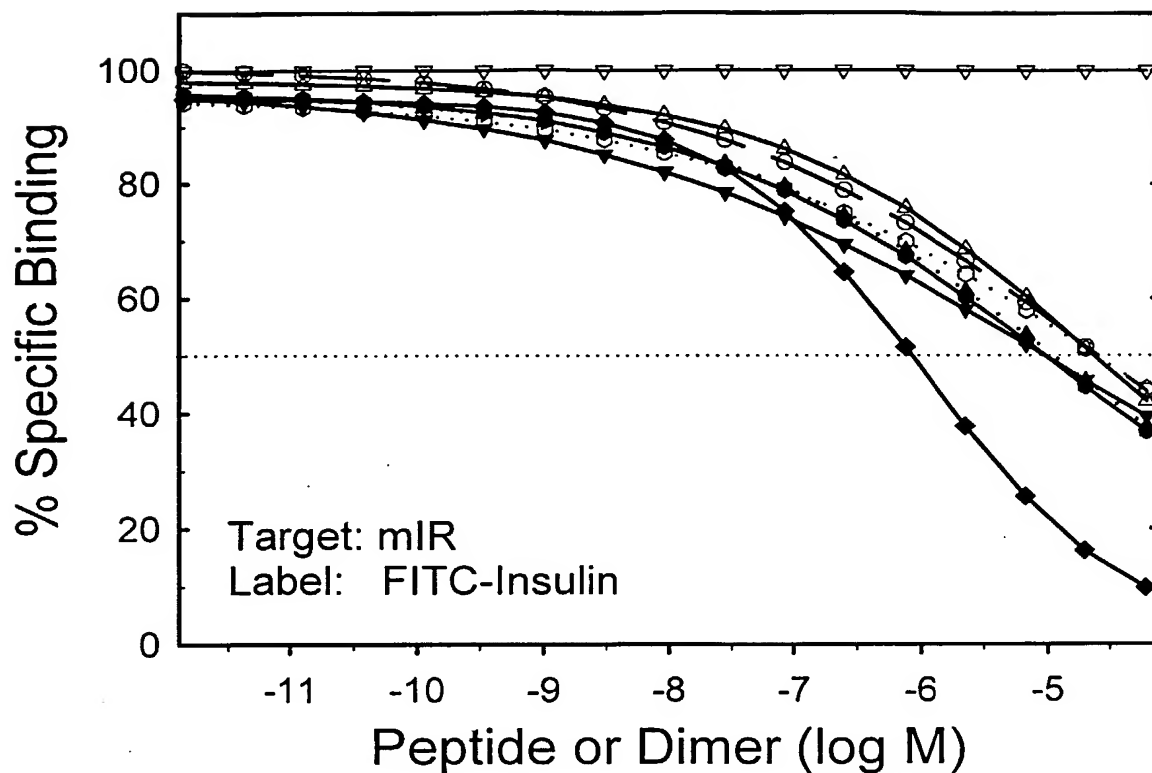


FIG. 26B

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FIG. 27A



Symbol	Peptide or Dimer	Sequence
△	H2C	FHENFYDWFVQRVSKK
□	S291	(Lig-GGG-H2C) ₂₋₉
▼	RP9	GSLDESFYDWFERQLGKK
■	S375	(RP9-Lig)- <u>14</u> -(RP9-Lig)
◇	S337	(RP9-Lig) ₂₋₂₃
○	S391	truncated(-GSLDE)RP9(-KK)
●	S390	truncated(-GSLD)RP9(-KK)
◊	S414	(truncated(-GSLD)RP9(-KK)) ₂₋₁₄
◆	S175	GRVDWLQRNANFYDWFVAELG
▲	S380	(EE-short-S175-Lig) ₂₋₉
▽	Linker <u>23</u>	

FIG. 27B

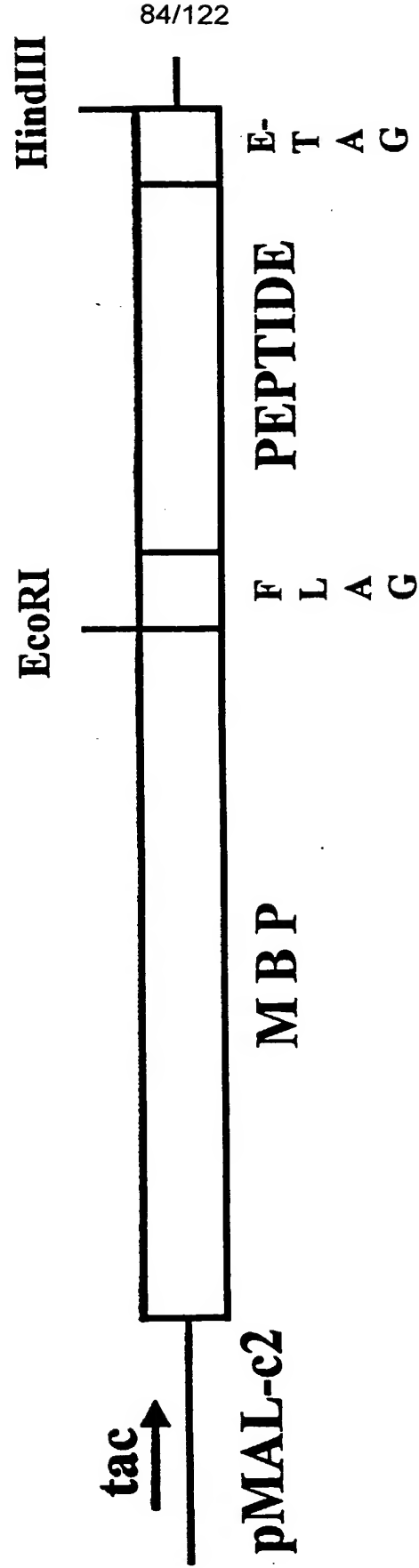
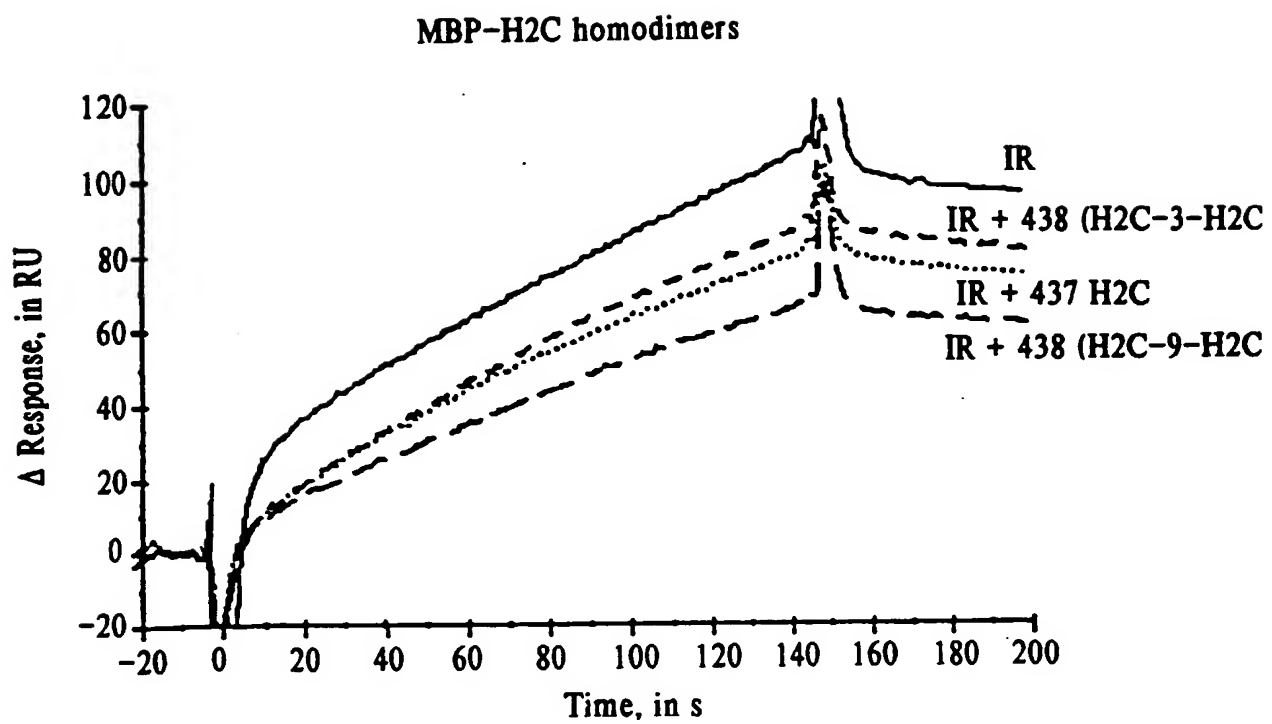


FIG. 28

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**FIG. 29**

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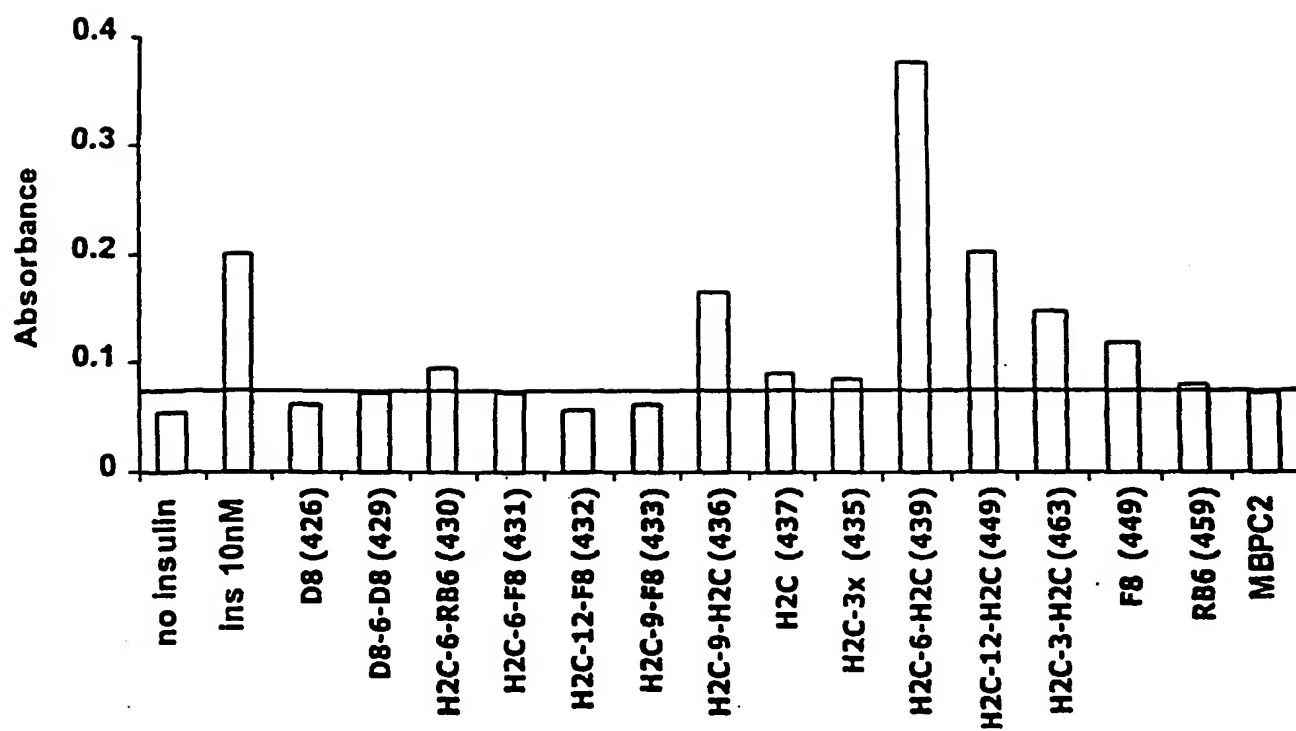


FIG. 30

FIG. 31A

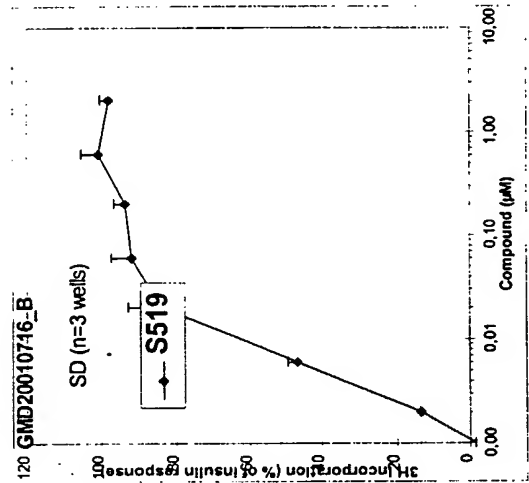
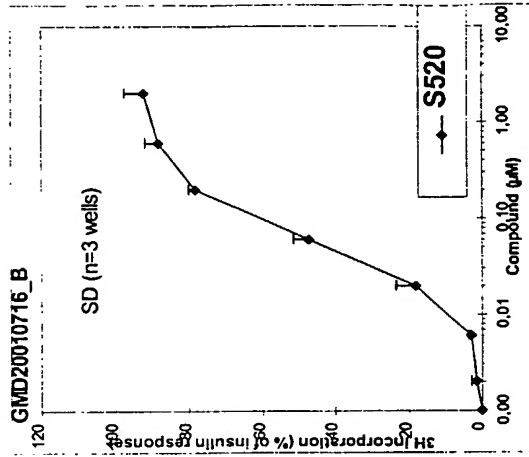


FIG. 31B

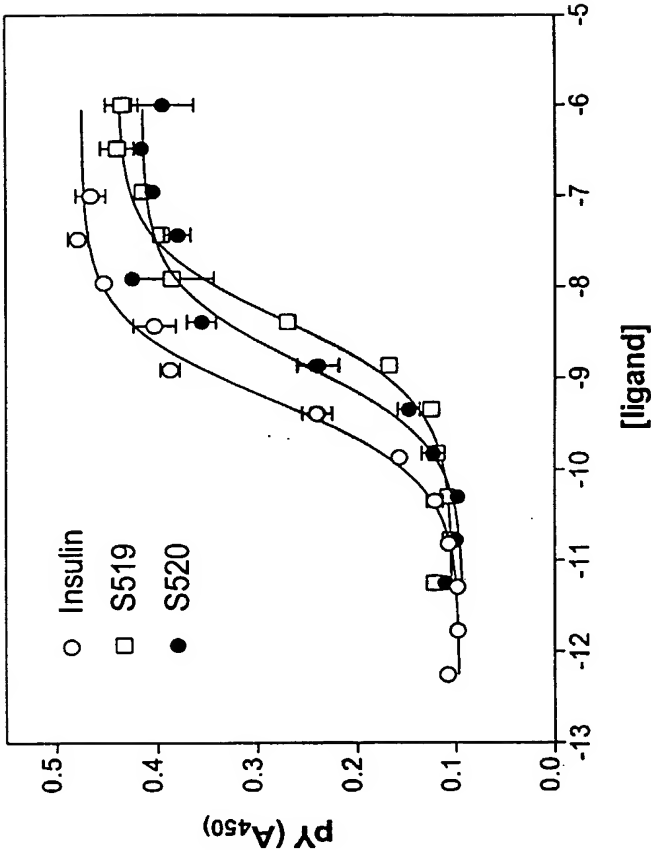


EC₅₀

- Insulin: 0.050 nM
- S519: 4.19 nM
- S520: 58.8 nM

FIG. 31C

FIG. 32A



Equation 1	Insulin	S519	S520
Best-fit values			
BOTTOM	0.09614	0.1038	0.09202
TOP	0.4740	0.4388	0.4145
LOGEC50	-9.237	-8.380	-8.852
EC50	5.8000e-010	4.1660e-009	1.4060e-009

FIG. 32B

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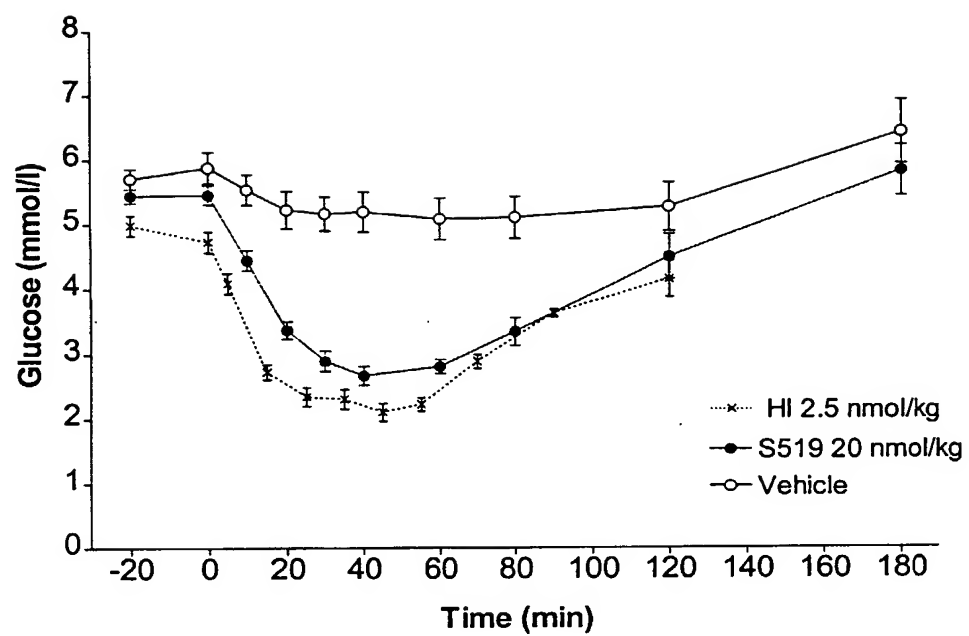
FIG. 33

FIG. 34A

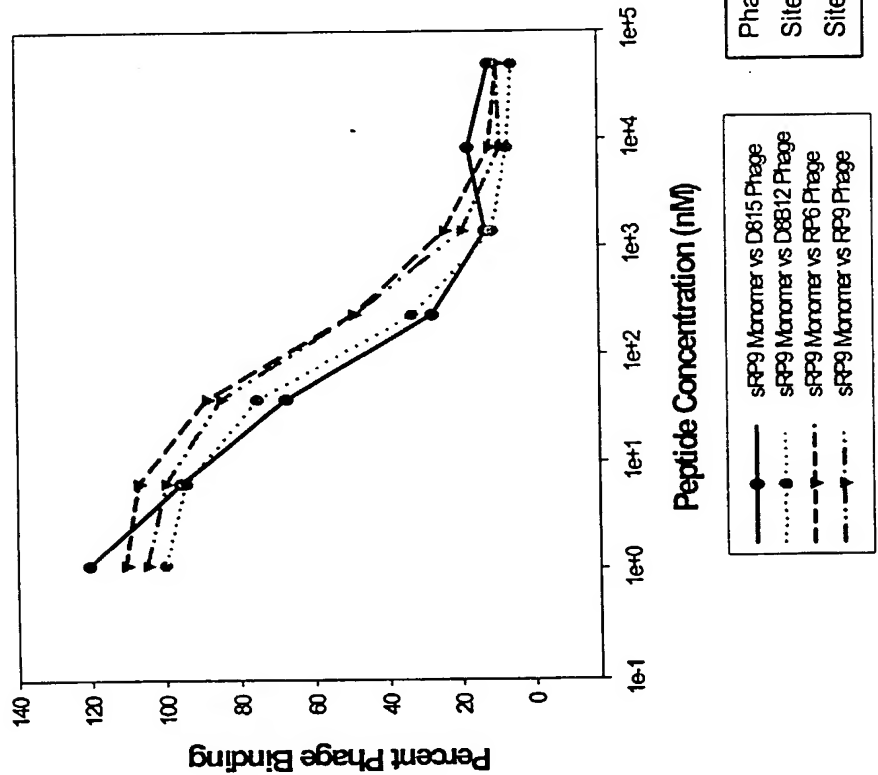


FIG. 34C

FIG. 34B

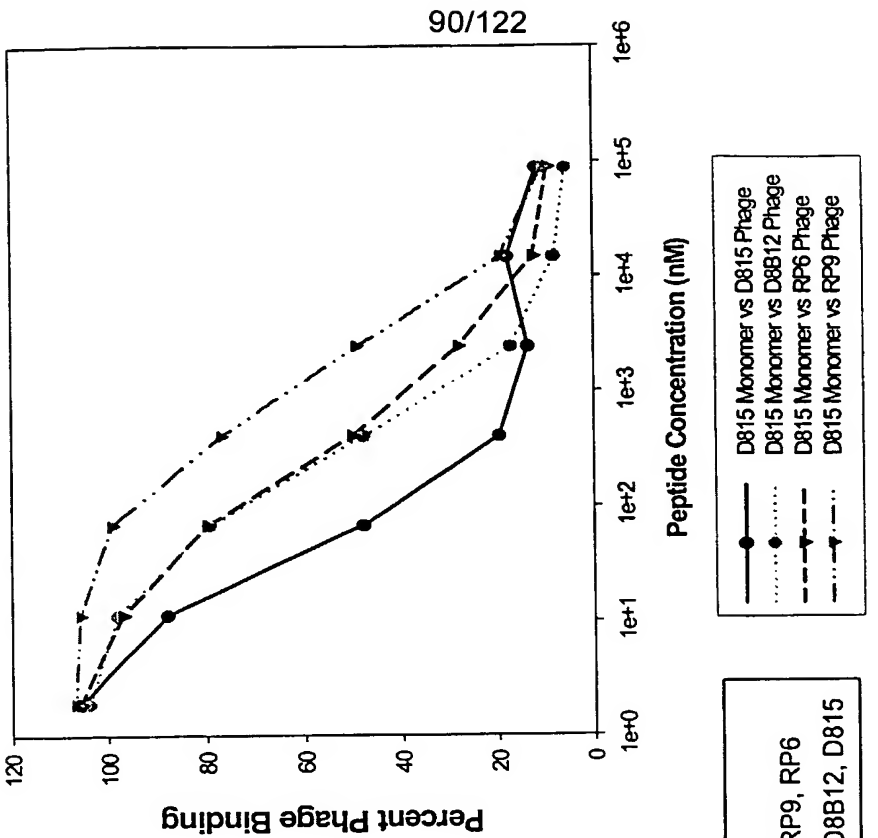


FIG. 34E

FIG. 34D

FIG. 35A

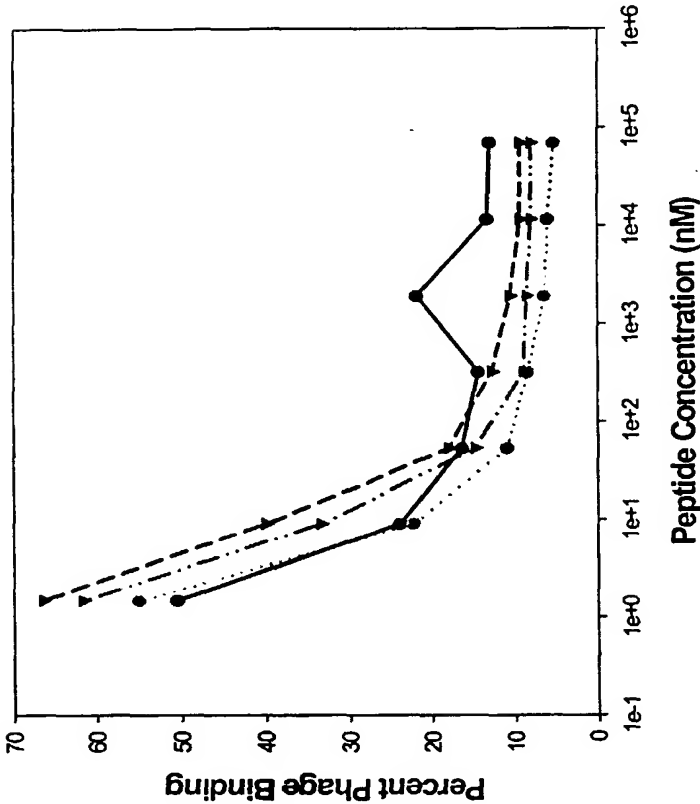


FIG. 35B

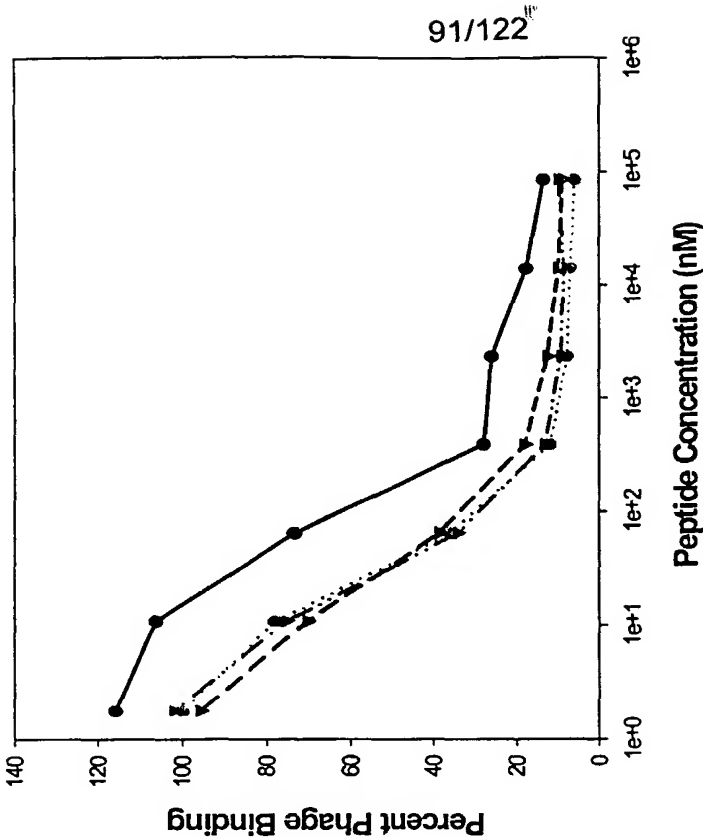


FIG. 35C

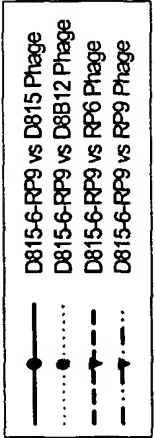


FIG. 35D

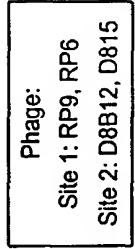
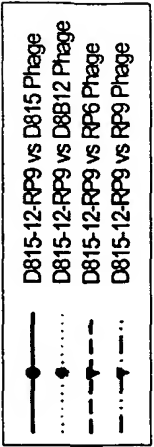
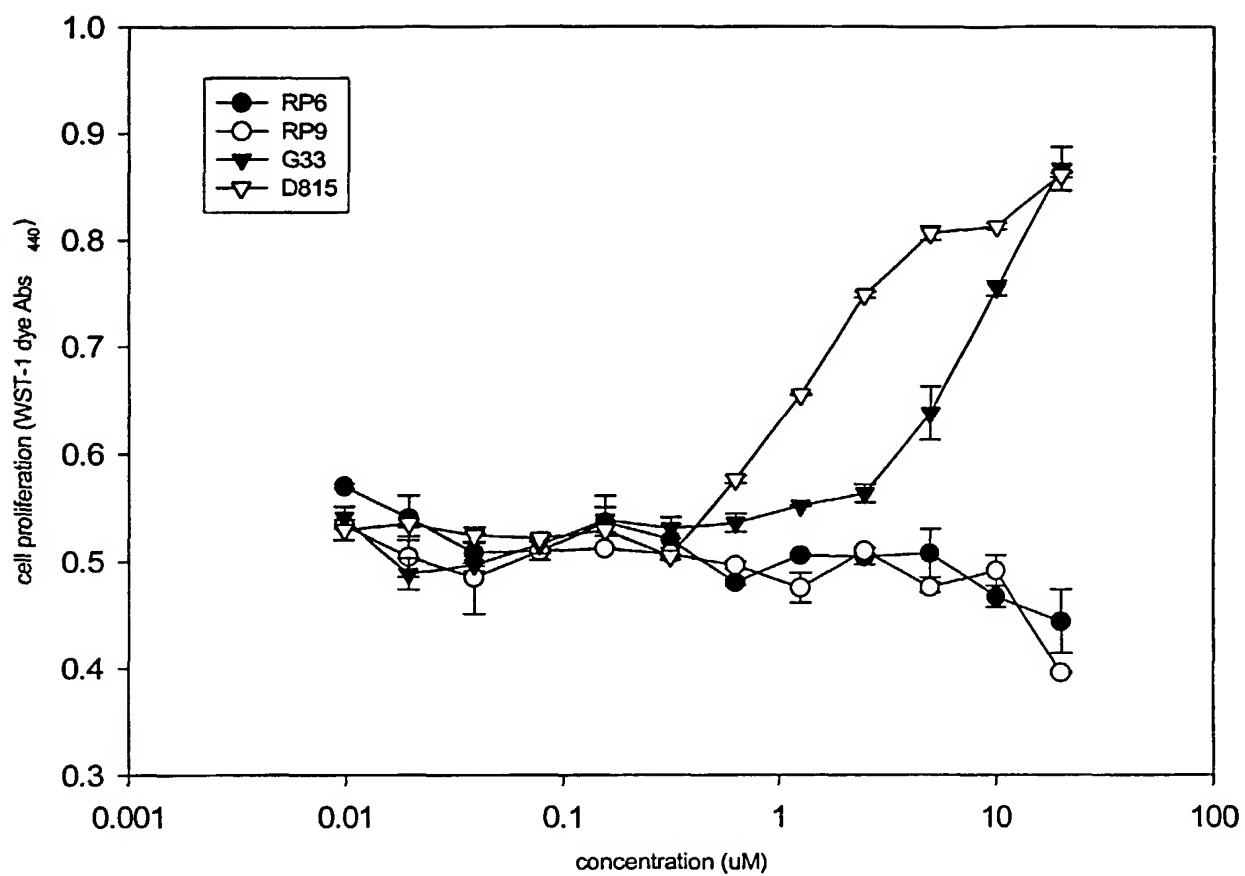


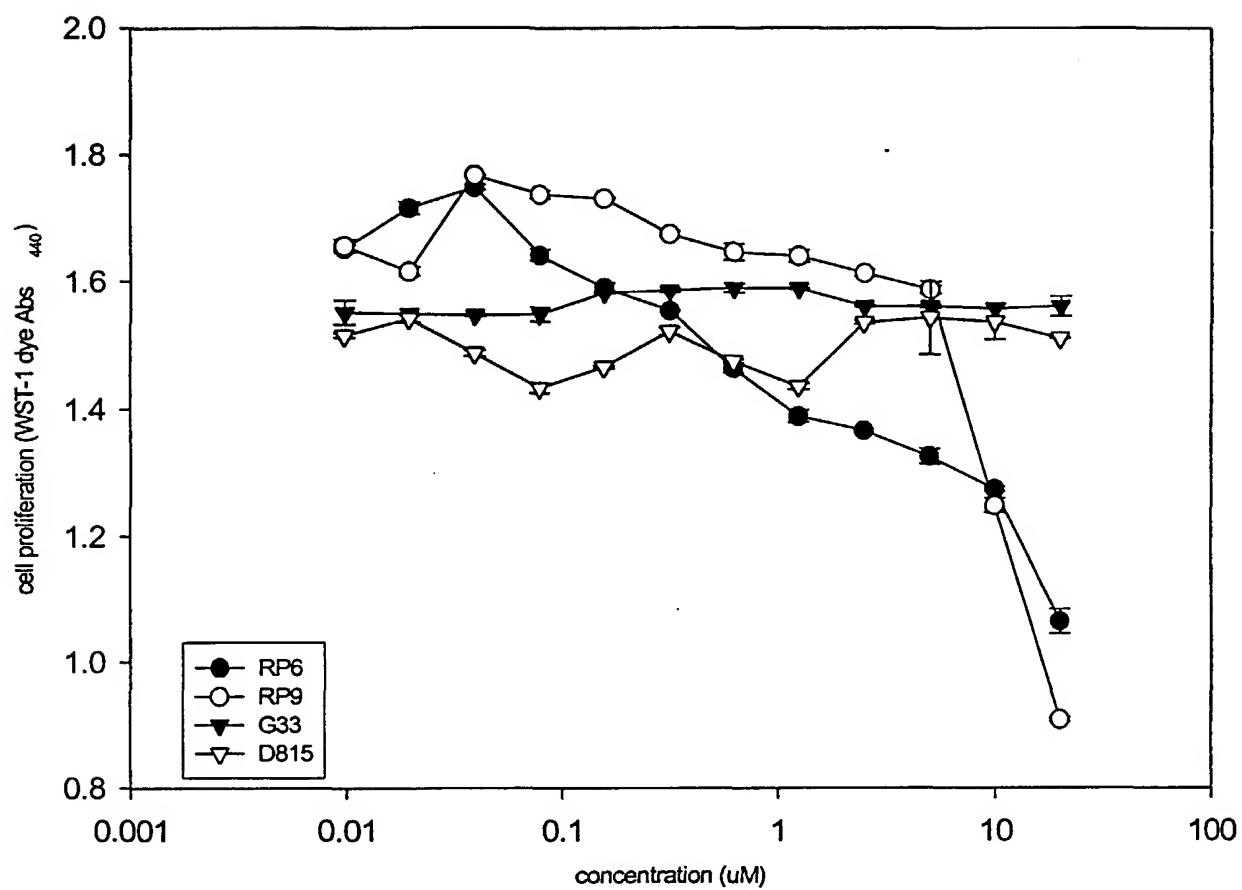
FIG. 35E



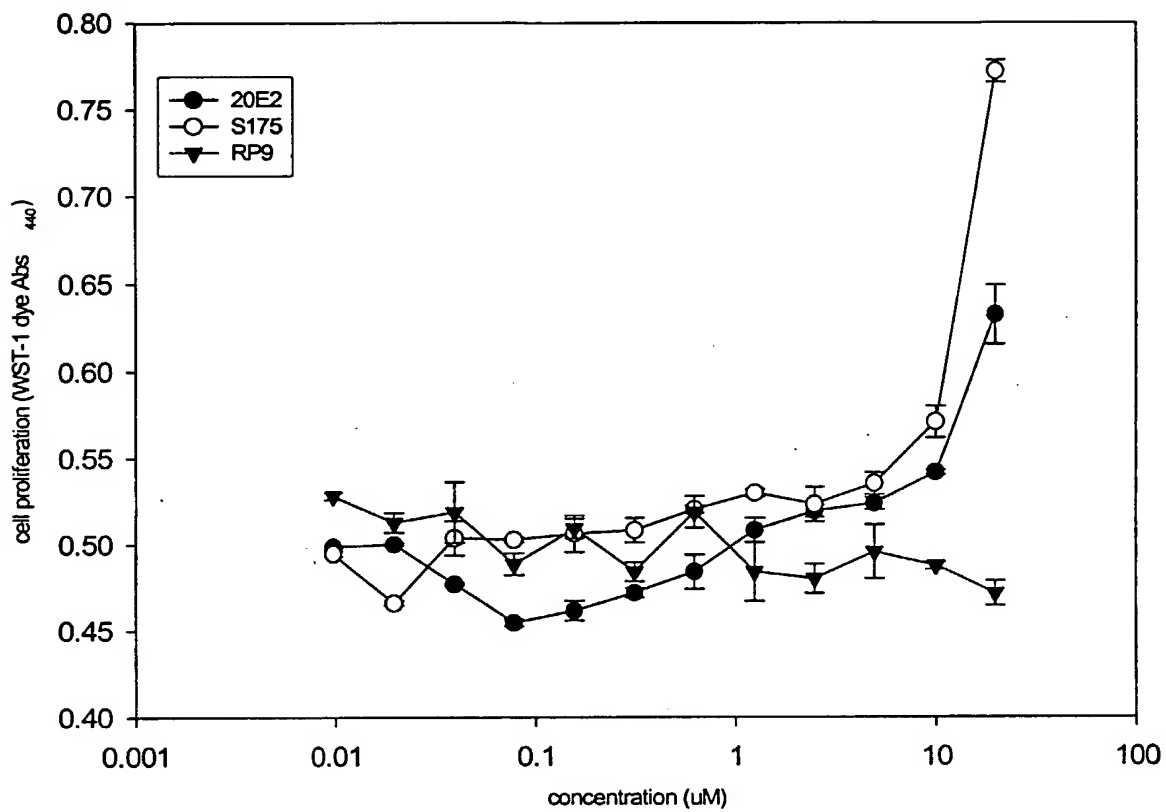
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FIG. 36

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FIG. 37

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FIG. 38

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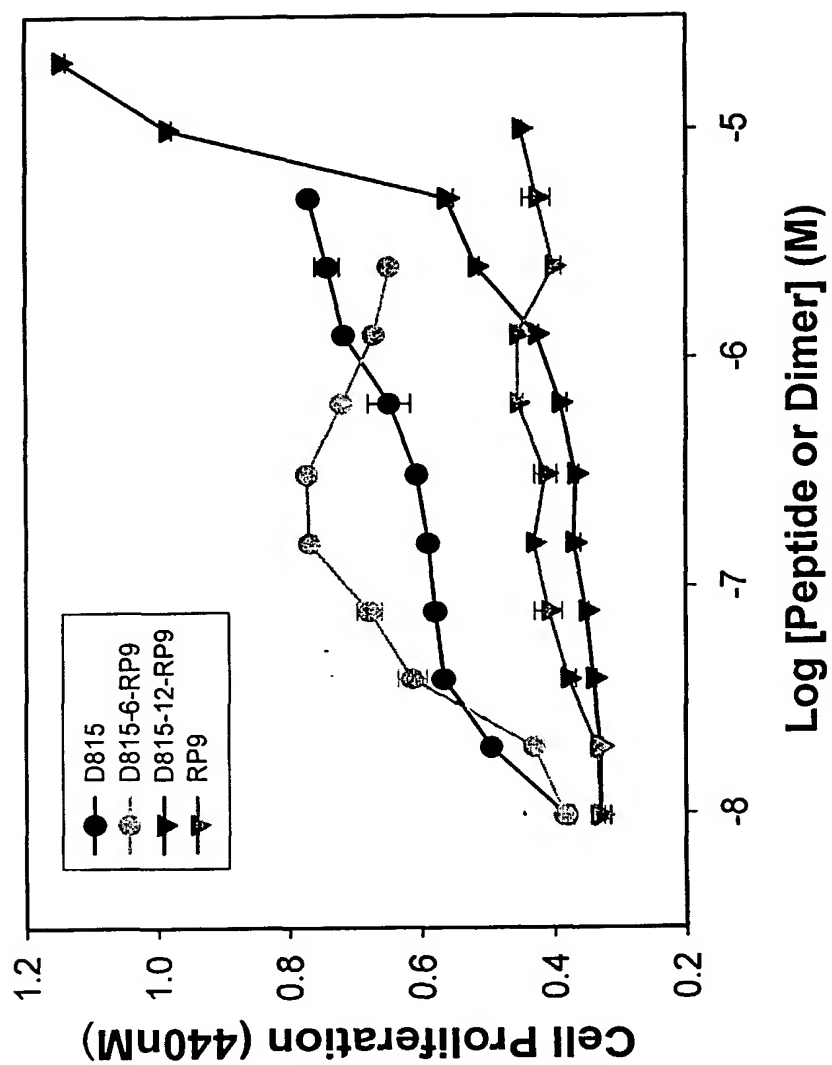


FIG. 39

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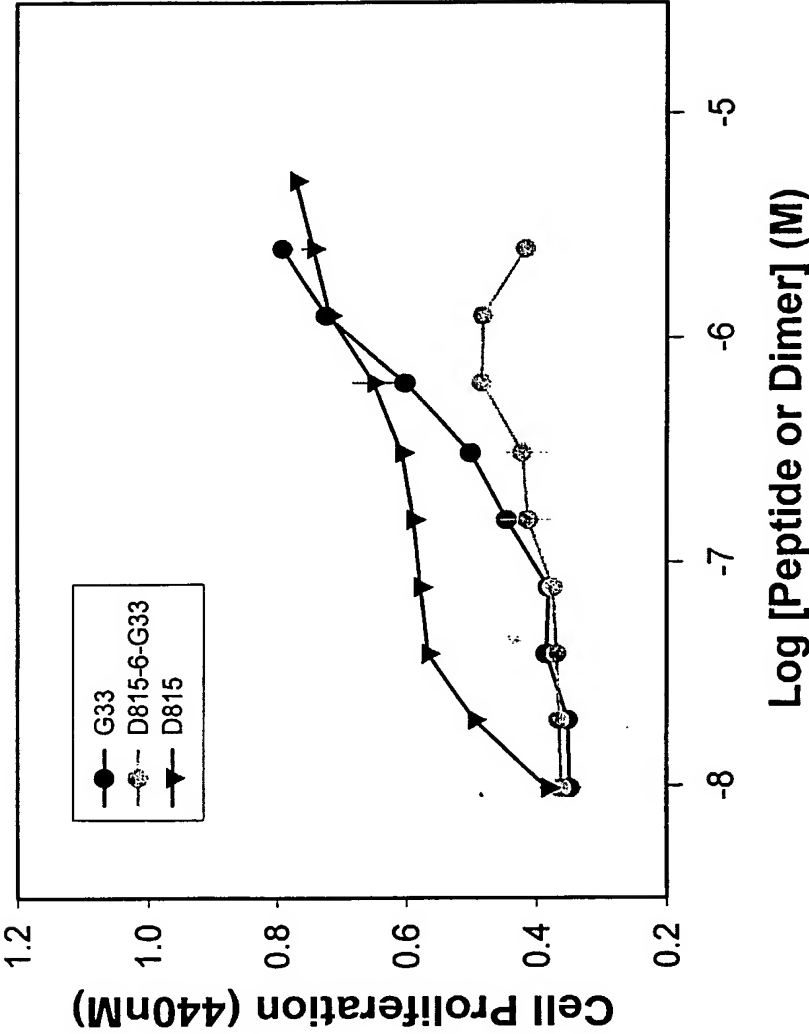


FIG. 40

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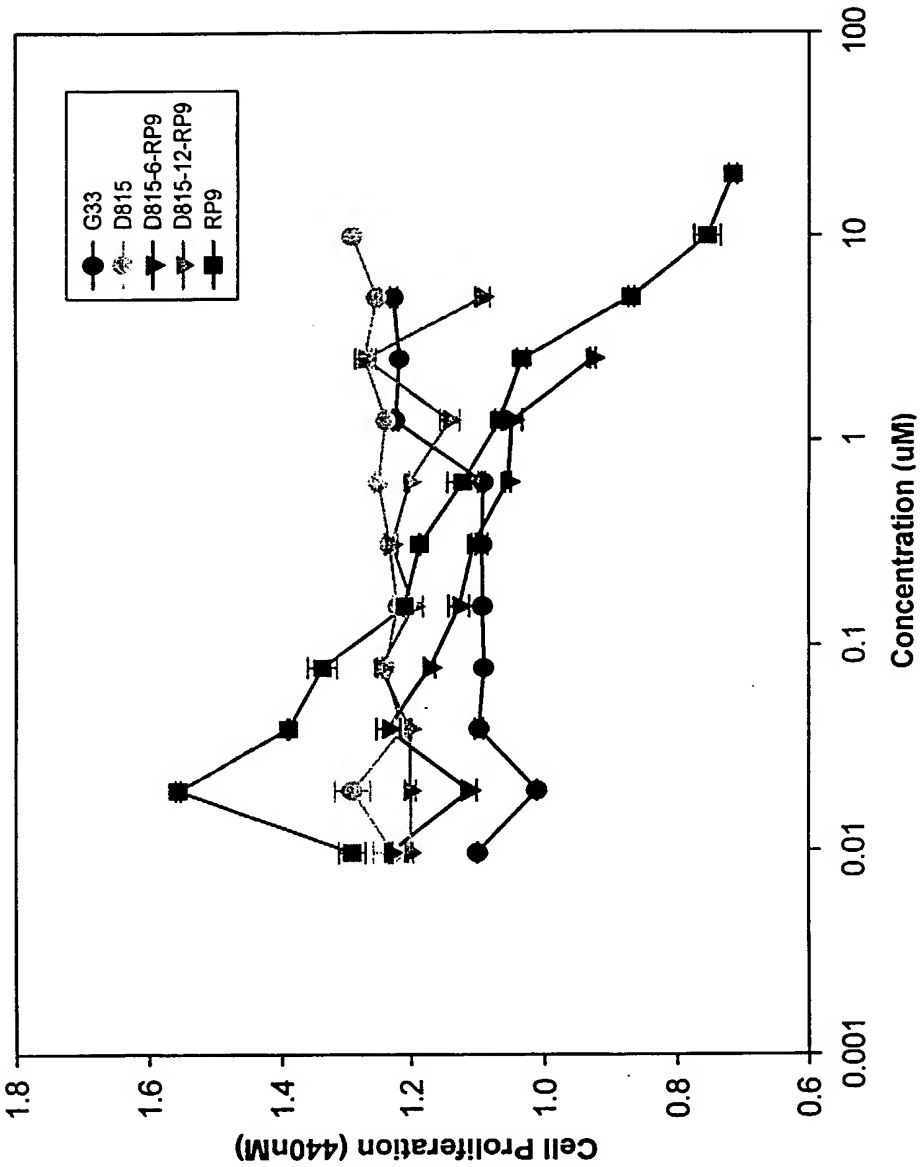
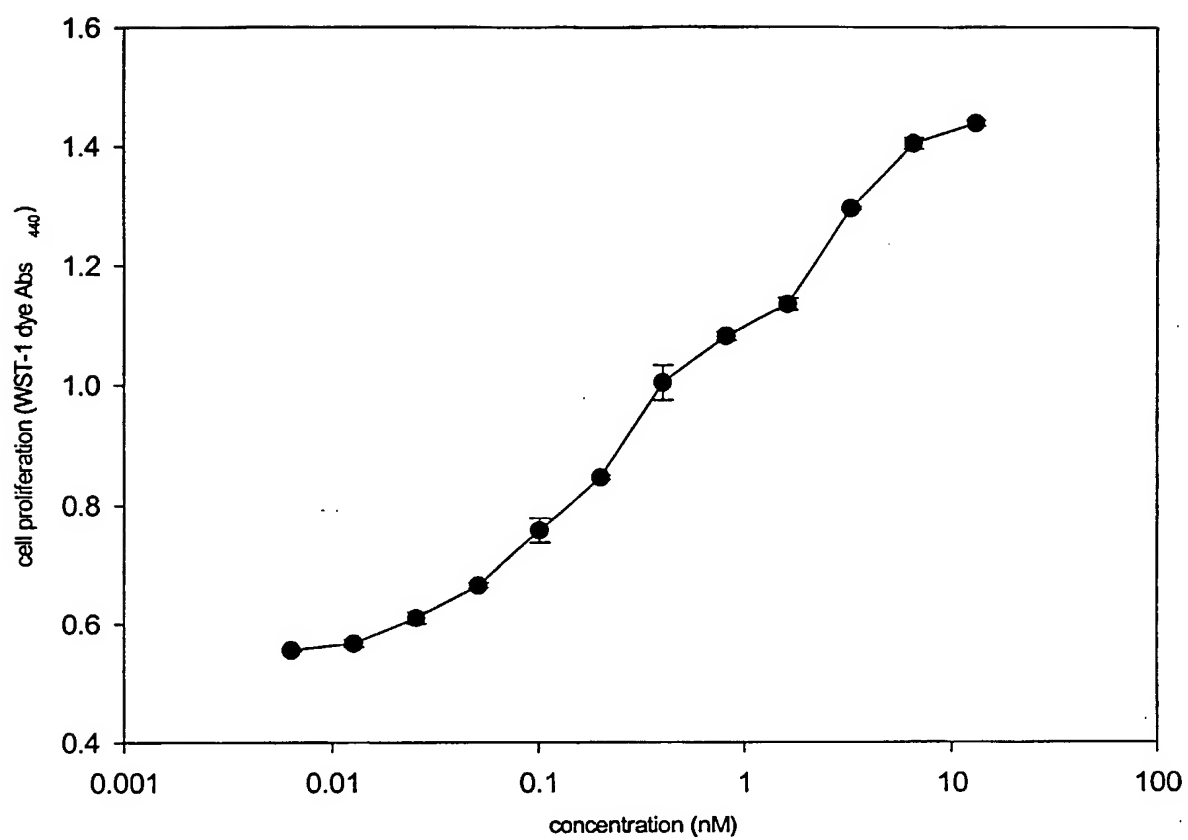


FIG. 41

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FIG. 42

Clone #	Sequence	Etag	IGFR	LDH	IGFR/LDH	Binder
IGFR-G33-4-A1		15.5	10.3	1.1	9.5	HIT
IGFR-G33-4-A2		4.8	2.9	1.2	2.5	HIT
IGFR-G33-4-A3		14.9	16.1	1.5	10.6	HIT
IGFR-G33-4-A4	PAMAVGYPOPCAKSTYERGRGSALESRCYQAAAAGAP	8.6	5.4	1.3	4.3	HIT
IGFR-G33-4-A5		23.5	12.1	3.4	3.6	HIT
IGFR-G33-4-A6		10.8	5.2	1.2	4.4	HIT
IGFR-G33-4-A7	MC	13.3	5.0	0.8	6.2	HIT
IGFR-G33-4-A8	PAMACKVC*CCSVSCYDGFPRSGAHPRRWAAAAGAP	6.0	1.7	1.0	1.8	CAND
IGFR-G33-4-A9	PAMAFKVSLSGSEFYEWFAGLVRDPTCGWTAAGAP	10.8	6.3	1.1	5.7	HIT
IGFR-G33-4-A10	MC	6.7	8.9	2.1	4.2	HIT
IGFR-G33-4-A11	AGHGACEFQVMFG*LVHLLGFPRLGKGLAAGA	5.8	5.8	1.2	4.9	HIT
IGFR-G33-4-A12	RPWRGSLRLVLGRRVECYCAERGATRGW*CAAAAGAP	3.3	2.6	1.1	2.4	HIT
IGFR-G33-4-B1	AGHGDGFGALSCKAAVAVVAVPVQTAGLRVRVAAAAGAP	8.1	3.2	1.2	2.6	HIT
IGFR-G33-4-B2	PAMAPRLYQGCPESEFYAWTAGHVSPALYGWAAAAGAP	4.8	4.1	1.1	3.8	HIT
IGFR-G33-4-B3	PGHGVSVRAGVSGMLRREVAG#CVSAWEGLCGRCA	6.4	2.0	0.9	2.2	CAND
IGFR-G33-4-B4	PAMAGMDPQ#CTVASSRWFAFPV#VWVRC#AAAAGAP	5.8	5.4	2.6	2.1	HIT
IGFR-G33-4-B5	PAMAGMFSQTCPEGFYGFAGQAQSDSSLCRAAAAGAP	15.8	2.5	0.9	3.0	HIT
IGFR-G33-4-B6	PAMAPLGFRCAGAY*VGCGRVAF#RCWAAAAGAP	7.7	2.3	1.2	1.9	HIT
IGFR-G33-4-B7	PAMAGILCPSCPHFLVDS#AAQDAAGQWPSAAAAGAP	7.2	3.3	1.2	2.8	HIT
IGFR-G33-4-B8	MC	4.8	1.4	1.0	1.5	
IGFR-G33-4-B9	PAMARRIPRECGDSFYVGLRWLVENPRSDWAAAAGAP	6.2	1.9	1.0	1.9	CAND
IGFR-G33-4-B10	PAMADRIQVQCPDSFYGWFAVQEPGTSGLAAAGAP	8.5	3.5	1.0	3.5	HIT
IGFR-G33-4-B11	PAMAGLPS*SCRVAMYKGQAAWSCSAAAAGAP	4.9	3.9	0.9	4.3	HIT
IGFR-G33-4-B12	RPWRLILVTLVREASMTGSGVWYPRRGAGPAEGA	3.6	2.6	1.0	2.5	HIT
IGFR-G33-4-C1		27.7	24.5	1.0	24.5	HIT
IGFR-G33-4-C2	PAMAGSARQVCVDGVVGVWREG*VVDQWL#RAAAAGAP	28.2	8.4	1.9	4.5	HIT
IGFR-G33-4-C3	PAMAGINQACEGGFTDCLWSLSGASSGRAAAAGAP	29.7	5.3	1.3	4.0	HIT
IGFR-G33-4-C4	RPWRVSSLRHVRVTCGELFGGVQVSELFCLECAAAAGAP	7.5	5.6	1.1	5.0	HIT
IGFR-G33-4-C5		4.5	4.4	1.2	3.8	HIT
IGFR-G33-4-C6	PAMAGLIYNSCLAYFDDLIERRLEKPG#RFAAAAGAP	36.1	22.9	6.3	3.7	HIT
IGFR-G33-4-C7	PAMAGINPQSCGETSGKCMRGQVSLRWWSAAAAGAP	10.0	1.7	1.1	1.6	CAND
IGFR-G33-4-C8	PAMAFILPRSCEDLYDFLASKVHVHFRSLAAAAGAP	9.7	6.9	1.9	3.6	HIT
IGFR-G33-4-C9	PAMACMSSQPCGESFYDWFAGQVDRDPGWESAAAAGA	23.3	19.4	9.5	2.1	HIT
IGFR-G33-4-C10	RPWRGWAIRGVRHRC*GAWRGQVQAQELCR#AAAAGA	30.2	9.3	4.3	2.2	HIT

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FIG. 43A-1

Clone #	Sequence	Etag	IGFR	LDH	IGFR/LDH	Binder
IGFR-G33-4-C11	PAMAGIASHTCPGGFYEWFAQSRAPGWDGAAAGAP	10.6	6.7	1.1	6.1	HIT
IGFR-G33-4-C12		19.2	30.2	5.2	5.9	HIT
IGFR-G33-4-D1	PAMAGRIARACPDMSFGLAGQGSQQSGWQAAAGAP	2.6	1.8	1.1	1.7	CAND
IGFR-G33-4-D2	PAMARPI SPLC#RRSKDEDA SRVSLPGFFCAAGAP	6.2	5.1	1.2	4.4	HIT
IGFR-G33-4-D3	MC	31.0	8.5	1.0	8.3	HIT
IGFR-G33-4-D4	PAMADYKDDDDKTFYACLASLMAGTPRQYTPWARCPAAAGAP	4.8	1.7	1.1	1.5	CAND
IGFR-G33-4-D5	MC	19.5	2.2	1.0	2.2	HIT
IGFR-G33-4-D6	RPWRVNTSECL#FVCSLFSGYECWVG*WAAAGAP	3.4	1.1	1.0	1.1	HIT
IGFR-G33-4-D7	PAMAGMGVQSCHDSFYGWFGCLFSDAEGDRAAGAP	20.7	15.2	7.0	2.2	HIT
IGFR-G33-4-D8	PAMAGDTSRACPESLNG.FCVVGVALRRRWIAAGAP	20.1	7.0	1.0	7.1	HIT
IGFR-G33-4-D9		14.5	6.6	1.7	3.8	HIT
IGFR-G33-4-D10	PAMARWWRGLCGERWYHRGWVQVQFPWERGAAAGAP	6.4	1.1	1.1	1.0	HIT
IGFR-G33-4-D11	RPWRVPWVLEMPYGNANLVFYDALQRLAAAGAP	27.7	19.7	1.2	16.5	HIT
IGFR-G33-4-D12	AGHGVCLAGVFGAELGGGRVSGFAIGQVRAAGAP	29.8	16.9	3.3	5.0	HIT
IGFR-G33-4-E1	PAMAGRIKEFCRSRFDYDQVACLKGPWSWGAAAGAP	11.0	13.2	2.0	6.5	HIT
IGFR-G33-4-E2	PAMAGRIKEFCRSRFDYDQVACLKGPWSWGAAAGAP	18.9	16.0	3.7	4.3	HIT
IGFR-G33-4-E3	PAMAGISSRSCAENLRFGRWQGSVDWDLAAAGAP	22.4	21.3	0.9	22.9	HIT
IGFR-G33-4-E4	PAMASRIPOWCRRDSFYEFWFECLLGPRESRAAGAP	14.5	7.3	1.2	6.1	HIT
IGFR-G33-4-E5	PAMAGAESCYRAKSFYDGLGCLVGEAWGGAAAGAP	7.8	14.3	1.9	7.4	HIT
IGFR-G33-4-E6	PAMARSGAPRCHDPFYEFWFAVEAQEPLRCEAAAGAP	6.0	3.1	1.0	3.1	HIT
IGFR-G33-4-E7	PAMAGMGVQSCHDSFYGWFGCLFSDAEGDRAAGAP	13.9	13.9	1.9	7.4	HIT
IGFR-G33-4-E8	PAMADISFESCLAQLLGNWRAGEGSKRLWRCAAGAP	11.9	17.1	3.5	4.9	HIT
IGFR-G33-4-E9	PAMANTFLYPCRDPPFYHSLADLVGVAMQCAGAAAGAP	23.2	24.5	5.2	4.7	HIT
IGFR-G33-4-E10	PAMARRIPRECGRDSFYAGRLCLVSPRSDWAAAGAP	9.4	5.8	1.7	3.3	HIT
IGFR-G33-4-E11	PAMASIVCPFCEDSFYNNFAAQVADTRGLWAAAGAP	24.1	33.5	10.1	3.3	HIT
IGFR-G33-4-E12		1.2	0.9	1.0	0.9	
IGFR-G33-4-F1	PAMAWSHSHAYTESYYDNFAAQVLSAGSGRAAGAP	0.9	1.1	0.9	1.3	HIT
IGFR-G33-4-F2	PAMAGRIKEFCRSRFDYDQVACLKGPWSWGAAAGAP	7.2	8.5	0.9	9.7	
IGFR-G33-4-F3	PAMARSPPACGDSFYGWFECEVSGLRGRRGAAAGAP	2.2	1.4	1.0	1.4	
IGFR-G33-4-F4	PAMAGISYPACEESFYDCLASLVSPWGSAGAAAGAP	12.1	5.2	0.8	6.7	HIT
IGFR-G33-4-F5	PAMAGRIKEFCRSRFDYDQVACLKGPWSWGAAAGAP	16.7	24.2	7.3	3.3	HIT
IGFR-G33-4-F6	PAMAVVAGQYCRDSFYDRLSALVGDWRCGAAAGAP	13.6	7.4	1.9	3.8	HIT
IGFR-G33-4-F7	PAMACTASRFCAVSFYEFWFAAQLPDLGGDSAAAGAP	12.5	16.9	1.2	13.8	HIT
IGFR-G33-4-F8	PAMAGITLQSCGGFFYELLASVVGDTCRLAAAGAP	20.2	10.9	1.0	11.3	HIT
IGFR-G33-4-F9	PAMAGYICRSCQGSFYGCCLAALVRDPRCSRAAGAP	24.7	33.0	8.8	3.7	HIT
IGFR-G33-4-F10	PAMAGRIKEFCRSRFDYDQVACLKGPWSWGAAAGAP	7.1	10.6	1.2	9.1	HIT
IGFR-G33-4-F11	RPWRVAGAPRCHDPFYEFWFAVEAQEPLRCEAAAGAP	1.0	1.0	0.8	1.2	

FIG. 43A-2

Clone #	Sequence	Etag	IGFR	LDH	IGFR/LDH	Binder
IGFR-G33-4-F12	PAMAGMGVQSCHDSFYGWFGLFSDAEGDRAAAGAP	7.6	4.7	0.6	8.0	HIT
IGFR-G33-4-G1	PAMASICGQSCRDPFYAGLRGLLLEPLQLGAAAGAP	17.6	18.5	1.0	19.5	HIT
IGFR-G33-4-G2	PAMAGVMSKCCSGSFYDNLADLVPEASWSWAAAGAP	6.5	5.7	1.0	5.5	HIT
IGFR-G33-4-G3	PAMASFSGEACGGSFYDCLAGLMRDSSVSRAAAGAP	18.4	7.9	1.1	7.4	HIT
IGFR-G33-4-G4	PAMASFSFYTCMETLLDGGGQAFNRCRRTAAAGAP	22.5	20.1	1.3	15.6	HIT
IGFR-G33-4-G5	PAMARVIYPTCPDRDFYGGLAALVFGPHVCGAAAGAP	22.8	21.7	1.9	11.5	HIT
IGFR-G33-4-G6	PAMAGISQACTDPFYWFEGLVSNGGWCRAAAGAP	5.9	5.3	1.2	4.3	HIT
IGFR-G33-4-G7	PAMAGRIKEFCRSFYDQVACLKVPKPSWGGAAAGAP	18.8	2.1	1.0	2.1	HIT
IGFR-G33-4-G8	PAMAGAESCYRAKSFYDGLGLVGEAWWGGAAAGAP	23.6	30.3	3.7	8.2	HIT
IGFR-G33-4-G9	PAMADMSQVCSQSMTGFRFSVDYDGLRCLAAAGAP	17.3	4.6	0.9	5.1	HIT
IGFR-G33-4-G10	PAMARRIPRECGDSFYAGRLCLVESPRSDWAAAGAP	26.8	24.6	5.4	4.6	HIT
IGFR-G33-4-G11	PAMARVIQEAACGGSFYDGLACLVPYQGWGAAAGAP	3.3	1.5	0.9	1.7	CAND
IGFR-G33-4-G12	PAMAGGRSVACQESFYALLGCVVMGPGGSAAGAP	24.1	32.1	12.1	2.7	HIT
IGFR-G33-4-H1	PAMAGISFRSCLQALIAGSAGNASEMGCRSAAAGAP	5.9	5.8	1.2	4.8	HIT
IGFR-G33-4-H2	PAMAGIRDSYCQGAFYDWFAGLVDDGLFCQAAAGAP	9.2	4.4	1.0	4.4	HIT
IGFR-G33-4-H3	PAMAGISYQSCEDSFYAWFACTVLDTRGGGAAAGAP	17.8	16.0	1.8	8.9	HIT
IGFR-G33-4-H4	PAMARVIYEACGGSFYDGLACLVPYQGWGAAAGAP	3.1	3.2	1.1	2.8	HIT
IGFR-G33-4-H5	PAMADMPLECLDPFYSWFAQQVSDPRFCGAAAGAP	20.1	7.5	0.9	8.0	HIT
IGFR-G33-4-H6	PAMARVIQEAACGGSFYDGLACLVPYQGWGAAAGAP	5.1	2.4	0.8	2.9	HIT
IGFR-G33-4-H7	PAMAGRIKEFCRSFYDQVACLKVPKPSWGGAAAGAP	12.9	11.1	1.1	9.8	HIT
IGFR-G33-4-H8	MC	23.4	23.5	1.6	14.7	HIT
IGFR-G33-4-H9	PAMAHISFHSCLALQDPEWGQPSAARNCAAAGAP	1.2	1.1	0.8	1.3	HIT
IGFR-G33-4-H10	PAMAMTAQESCPDSFYECCLAVLVGDRWGGWAAAGAP	7.9	10.4	2.8	3.7	HIT
IGFR-G33-4-H11	PAMAHISFHSCLALQDPEWGQPSAARNCAAAGAP	16.8	23.7	1.3	18.1	HIT
IGFR-G33-4-H12	PAMAGTISQCCEENFYAGLAHLAHLAGVGWGCAGAAAGAP	20.4	19.0	4.7	4.0	HIT

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FIG. 43A-3

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Clone #	E-Tag	IGFR	IR	Sp/Irr	Binders
B10	DDKTFYACLEFLLSGNPEGSGPWDRCR	29.0	1.0	29.0	HIT
D1	MC	17.0	1.1	25.1	HIT
A4	DDDKIFYSCLASLLHGGPQRTGWPWERC	25.2	1.0	25.6	HIT
A6	DDDKTFYSCLASLLTGPREQNRGAWERC	23.3	1.1	21.2	HIT
B1	DDDKSFYSCLASLLTASRLPSRGAWDGC	22.8	0.9	25.3	HIT
E4	DDDKSFYSCLSLLTGAPQPIRGAWDRCR	20.6	1.1	19.1	HIT
C11	DDDKSFYSCLASLWSGTGSSRGWRWECR	20.4	1.3	16.2	HIT
C2	DDDKTFYSCLGALLAGTGERNLRPWGRCR	19.1	1.0	19.1	HIT
B6	DDDKTFYSCLSLLTGSPDKRGPWGGR	19.0	1.2	15.3	HIT
A12	DDDKTFYKCLASVLGTSTQTKRRPWEGCR	18.8	1.0	18.4	HIT
D2	DDDKPFYSCLATLLTDPQSQRGAWGRCR	17.2	1.1	16.1	HIT
C1	DDDKSFYSCLAALLTGSSQSGGAWMLCR	16.9	1.1	15.2	HIT
F10	DDDKSFYSCLASLVAGTPWPKGGSWERC	16.6	0.9	18.2	HIT
B11	DDDKSFYSCLASLVGTIPRSNSGTQVFCR	16.1	0.8	20.8	HIT
A9	DDDKSFYSCMASLLTGTPESSRRGMGERCG	15.9	1.3	11.8	HIT
A10	DDDKAFYSCLASLLTGSPPAQGGPWDRCR	15.6	1.0	16.2	HIT
B9	DDDKFFYSCLASLLSDTPQRRRPGVRCR	14.3	0.9	15.4	HIT
A3	DDDKTFYSCLASLLAGNPQNRAGWEYCR	13.3	0.9	15.1	HIT
F2	DDDKTFYSCLSLLLGPPQKNPQPGERC	13.3	0.9	14.8	HIT
A7	DDDKMFYSCLESLLIGRWPRNGGSLSRCR	13.2	1.1	12.5	HIT
G3	DDDKSFYSCLTFLLTGTQANDASWERC	13.2	1.0	13.8	HIT
A11	DDDKSFYSCMAALLSGAPQKSRGWERC	12.7	0.8	15.0	HIT
B7	DDDKAFYRCLAYLLAGRPQASGGGVRCR	12.5	0.9	13.5	HIT
D5	DDDKAFYSCLAALRERSPQMSRGTWGGCR	11.8	1.3	9.3	HIT
E8	DDDKTFYACLAALLGGTAELHDGSLRCG	11.8	1.3	9.0	HIT
D10	DDDKTFYSCLSLLTGTLPARGARNICR	11.6	1.0	11.6	HIT
D8	DDDKTFYSCLSLLAGSPLPRDLWAGCR	9.2	0.9	10.6	HIT
D12	DDDKAFYSCMASLLAGTPEAQGSWVRCR	7.4	0.8	9.0	HIT
A5	DDDKNFYACMESLVSVAPPSSRDPFECRR	7.3	1.3	5.5	HIT
F6	DDDKSFYSCLASLVSGTA.PNRGPWERC	6.9	1.0	7.1	HIT
G5	DDDKIFYSCLASLLDDTAQSRGQWARC	6.4	1.3	5.1	HIT
C6	DDDKIFYSCLGALLSGTPQTSHTSGRCR	5.9	1.1	5.4	HIT

FIG. 43B-1

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Clone #	E-Tag	IGFR	IR	Sp/Irr	Binders
D3	TDDKTFYFCLASLLAGTQQQSRGAWERCG	5.1	5.9	0.9	HIT
A2	DDDKAFYSCLASVLTGSPHGRSRWERCR	18.6	5.5	0.9	HIT
B2	DDDKTFYSCLESMLTGTPPCRGHGERGR	8.0	5.5	1.0	HIT
D7	DDDKTFESCLEALVSGSRRLRGLWYRCR	10.6	5.5	1.1	HIT
C12	DDDKAFYSCLSLLAGTRERHRTWPRCG	12.0	5.3	1.0	HIT
B5	DDDKTFHSCLAALVTGTPQKRGPRWERCR	20.0	5.1	1.3	HIT
E2	DDDKTFYLCASLQTVTRLGDRVPWERCR	18.0	4.6	0.7	HIT
F3	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	3.7	4.5	1.4	HIT
H2	DDDKSFYSCLASLSNCTPGLLRQWEGCR	7.2	4.4	0.8	HIT
B4	DDDKTFYSCLSLLASTPQPNRGAWLCRR	11.9	4.3	1.2	HIT
G12	DDDKSFYSCLASLSNCTPGLLRQWEGCR	2.2	4.2	1.0	HIT
F5	MC	8.4	4.0	0.9	HIT
A1	DDDKTFYSCLGALLSGAPQTYRGPAGCR	8.1	3.9	1.0	HIT
E11	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	4.9	3.8	1.0	HIT
F9	DDDKHFYSCLSLLTAPPQSTRGPAGRHC	3.9	3.7	1.0	HIT
E3	DDDKTFYSCIASLLNGTQPNGGQWVRCR	1.7	3.6	0.8	HIT
G4	DDDKVFYTCIASLSTGTQORQSGEWQCR	9.4	3.3	1.3	HIT
E5	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	4.6	3.2	0.9	HIT
C10	DDDKPFYSCIASLIQGTPLPERGMWERC	6.3	3.0	1.0	HIT
C7	MC	10.6	2.9	1.0	HIT
H5	DDDKTFYSCVSWLLTGARQDGVWERC	5.5	2.9	1.3	HIT
H3	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	4.6	2.8	1.1	HIT
C3	DDDKAFYGCCLAALLTGARQPSRGVGERCF	6.0	2.7	1.5	HIT
F1	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	1.5	2.6	0.8	HIT
B3	DDDKTFYSCIASLLAGSPQKRGAGWEYCR	8.6	2.5	1.0	HIT
D11	DDDKPFYSCLESIVTGRPQADRGVWERC	4.9	2.4	0.9	HIT
E10	DDDKTFYSCVLSLRSAGHLSGRWERC	5.0	2.3	0.9	HIT
F12	DDDDKTFYFCLATLLTGPPVNPREPWACYR	2.5	2.2	0.8	HIT
D4	DDDKIFYSCVSLTGTNPPEVPGPFDRCG	3.0	2.1	1.1	HIT
E6	DDDKTFYSCLVSLNGTAKPNRGQWEGCR	2.7	2.1	1.4	HIT
F11	DDDKSFYSCVASLVNEGSPQVGLGERCR	3.5	2.1	1.2	HIT
A8	DDDKTFYSCLASMLTGPHPDRVPWDRCR	8.3	2.0	1.0	HIT
F7	DDDKKFYSCVSLVNGTSPARGLWERC	2.7	2.0	1.0	HIT
F8	DDDKVFYSCLESIVSGTPEVNGRAWERC	2.0	1.8	1.0	CAND
E12	YDDKRFYCYCLASLQTLQTNREQWERC	1.0	1.7	1.0	CAND
H1	DDDKTFYSCLESLLNGTQPNRGQWDPCS	1.9	1.7	0.9	CAND
H8	DDDKTFYTCIQLALITGYERPVGGRWESCR	1.2	1.7	1.2	CAND

FIG. 43B-2

Clone #	E-Tag	IGFR	IR	Sp/Irr	Binders
G9	1.5	1.6	1.1	1.5	CAND
D6	1.3	1.5	1.1	1.5	CAND
H6	3.2	1.5	1.3	1.1	
E7	3.2	1.4	1.1	1.3	
F4	1.4	1.4	1.2	1.1	
G6	1.4	1.4	1.0	1.5	
G11	1.6	1.4	1.0	1.4	
H4	4.7	1.4	1.0	1.4	
B8	9.1	1.3	1.0	1.3	
C8	7.7	1.3	1.4	1.0	
E1	2.3	1.3	0.9	1.4	
G10	1.2	1.3	1.2	1.2	
H10	3.5	1.3	1.0	1.3	
H11	2.6	1.3	1.0	1.3	
D9	1.1	1.2	0.9	1.3	
E9	1.1	1.2	1.1	1.1	
C9	1	1.1	1.1	1.0	
G1	0.9	1.1	0.9	1.3	
H7	2.2	1.1	0.9	1.1	
H9	3.1	1.1	1.1	1.0	
C5	3.3	1.0	1.0	0.9	
G7	0.9	1.0	0.9	1.1	
H12	3.7	1.0	1.0	1.1	
C4	1.1	0.9	0.9	1.0	
G8	0.7	0.9	1.0	0.9	
G2	1.1	0.8	1.0	0.8	
B12	9.3	13.2	0.7	18.3	HIT

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FIG. 43B-3

<u>IR</u>	Clone	Sequence	E-Tag	IR	IGFR	IR/IGFR	IGFR/IR
	B5	FHENFYDWFARKDSGGSGGSDLCVLEELFWGDSLFDYCTG	17.0	16.9	0.5	35.8	0.0
	A3	FHENF.DWVVRQVSGSGGSGNLCVLEELFWGASLFGECSG	13.0	11.8	0.3	35.8	0.0
	A8	SHGNFSEWVVRQYGGSGGSDLCVLEELYWGASLFGYCSG	13.2	13.1	0.4	33.2	0.0
	C7	FQESFYDWFVR.VTGGSGGSDLCGVEDLVWGSALSGYCAG	15.1	14.7	0.5	30.6	0.0
	B4	FHENFNDWFVREVSGSGGSDLCVLEELFWGASLFSYCSG	13.2	11.7	0.4	27.6	0.0
	B11	SHENFYDWFVR.GPGSGGSGSHLCVLEELFWGDSLFGACPG	10.9	9.1	0.3	27.0	0.0
	A9	FHENFYDWFARQVSGSGGSHLCVLEELFWGASLFA.CSD	10.7	12.3	0.5	25.7	0.0
	A6	FPDNFYDWFVR.VSGSGGSGSHLCVLEELFWGASPFYCSG	11.6	8.7	0.4	19.8	0.1
	A4	FQENFYDWFGRQISGGSGGSLCDVEELFWGVSLFGYCTG	13.6	12.1	2.6	4.6	0.2
	C8	FQENFYDWFVR.ASGSGGSGSHLCALVEEQFWGSSQFRYCSG	16.0	14.5	3.2	4.5	0.2
	A10	FHENFYDWFARQVYGGSGGSHLCVLEELF.GASLFATCSD	10.6	6.0	1.5	3.9	0.3
	D11	FHENFYDRIVRQVAGSGGSGALCVREELF.GDSLFGDCSG	12.4	5.5	1.5	3.6	0.3
	D4	FHKNFYDWFDRQVSGSGGSSRLCDLEELFWGASL.GHCSG	15.4	9.8	3.9	2.5	0.4
	C1	FHENFYDWFIRQDSGGSGSHLCAFEELGGASPFYCSG	16.8	2.7	1.3	2.1	0.5
	D12		11.7	8.7	4.6	1.9	0.5
	D8	SNENFYDWFDR.VSGSGGSGSHLCLLEELSWGASLFGYCYG	15.8	9.6	7.4	1.3	0.8
	C11	FHESFYDWFDRQVSGSGGSHLCVLEE.ELGASVFGCCSG	11.0	5.8	5.4	1.1	0.9
	C4	FHETFYDWFDR.VSGSGSGEELFGGASLFGYPSG	16.7	13.2	15.0	0.9	1.1
	D1	SHENFYDWFGRQVSGSGGSGSNLCDLDEVS.GASLCGYRSG	16.2	5.5	7.1	0.8	1.3
	C6	FH.NFYDWFCCQVPEWIPMTLAVLTCAVLEEPIWGDSLFGYG.E	16.1	1.7	2.2	0.8	1.3
	A5	SHENFYDWFVRQV.GGSGGSGSHLCDLEELGGASLMGSCSG	16.0	8.7	12.9	0.7	1.5
	B8	SHENFYDWFVR.VSGGAAAGAPPAMASHENFYDWFVR.VSGG	15.2	8.9	13.9	0.6	1.6
	D2	FHENFYDWFIR.VGGSGGSGSDLCVLEDDCSRAAAGAP	13.9	8.4	13.1	0.6	1.6
	A2	DYKDASVSGTFHDAFYEFWFR.VGS	13.4	6.9	12.6	0.6	1.8
	C12	FHENFYDLVPSAGSWIRWLWRF.PVRLGRTVLGCFSDR.LFW	9.2	4.4	6.8	0.6	1.5
	B9	FHENFYDWFDRQVSGSGSVRAAAGAP	17.8	8.2	16.3	0.5	2.0
	B1	VHENFYDWFDRQVSGSGGSQLCDL.EVIWGASLFGYCTG	18.1	7.3	13.4	0.5	1.8

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FIG. 44A-1

Clone	Sequence	E-Tag	IR	IGFR	IR/IGFR	IGFR/IR
B2	FHENFYDWFDR.VSGSGSGSGGSHLCVPPEQFWGASRFGYCSA	16.2	7.0	13.6	0.5	1.9
D9	FHDNFYDWFVRQVSGSGSGSGSRQCQASL.GYCSG	17.0	6.6	13.8	0.5	2.1
D5	OUT OF FRAME	16.1	4.8	10.5	0.5	2.2
C9	FHEDFYDWFVR.VPGSGSGSGGSHLCVPGYCSSL	17.2	5.1	14.2	0.4	2.8
B7	FRENFYDWFVC.VSGSGSGSGGSHLCVLEEAAGAP	15.9	4.0	10.6	0.4	2.7
D6	OUT OF FRAME	15.6	4.2	12.8	0.3	3.0
C5	GHDNFYDWFVRQVSGSGSGGSHLCV.GAFPWGYCSD	15.2	3.6	10.7	0.3	3.0
D3	FH.NFYDWFVRQVYGGSGSGGTGAAAGAP	16.2	3.5	12.0	0.3	3.4
C10	BAD SEQUENCE	11.2	2.5	7.6	0.3	3.1
A7	FHENFYDWFGRQVYGGSGSGGSPVCILGELS.GGALFGDCSG	15.5	1.8	5.1	0.3	2.9
A12	FHENFYDWFVR.LSGSGSGSGGSHLCVPEERLWGDPLFGYCSG	8.7	1.2	3.5	0.3	3.0
D7	FH.NFYDWFVRQVSGSGSGGSHPAR	16.2	3.0	11.9	0.2	4.0
A11	FHENFYDWFVRQVTGGSGSGGSHLCVLEELS.GAALPGYCSG	11.8	1.0	4.0	0.2	4.1
D10	VQGSFYDWFVRQVSGSGSGGSHLC.GSG	12.7	1.0	6.3	0.2	6.6
C3	FHENFYDWFVRQVSGSGSGGSHRCDVEELH.CASG	16.8	0.6	2.5	0.2	4.2
A1	DYKGGYWGSEYEGLM.LVQSGTSG	13.6	1.7	12.5	0.1	7.1
B6	OUT OF FRAME	12.7	1.0	8.1	0.1	8.1

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Non-Binders:

B12	FHENFYDWFDRQVSGSGSGGSHRCLVEERFWGASLFG.CSG	7.8	0.5	1.6	0.3	3.3
B10	SHENFYDWFVHQVSGSGSGGSHLCVLEERF.GPSLFGYCSG	10.8	0.6	1.4	0.4	2.3
B3	FHANFYDWFVRQVSGSGSGGSDLCVLQDMF.GGSGAAAGAP	16.9	0.7	1.2	0.6	1.7
C2	FQDNFYDWFVRQISGGSGSGGSHLCVLESWF.GASLFGYCSG	14.8	0.5	0.8	0.6	1.7

FIG. 44A-2

IGFR

Clone	Sequence	E-Tag	IR	IGFR	IR/IGFR	IGFR/IR
H11	PHETFYD.LGRLVFGSGGGSHLCVPEELFWGTSLLSYCSG	9.3	0.4	4.0	0.1	11.4
F11	FHENFYDWFVRQVSGSGGGSHL.GSG	12.5	0.8	5.2	0.2	6.5
E2	FHENFYDWFVRQVSGSGGGSHRCGLEEPV.GASLVGYCAG	13.4	1.3	7.5	0.2	5.7
G7	FHANFYDWFVRQV.GSGSGSGSG	16.1	2.1	9.8	0.2	4.7
G12	FHEDFYDWFVRQVSGSGGGSHLCVREELF.GASLLGDCSG	9.4	1.2	5.5	0.2	4.6
H7	.HENFYDWFVRQLSGSGGGSDGSHLFGYGSG	7.2	0.6	2.7	0.2	4.5
G11	OUT OF FRAME	11.4	1.4	5.8	0.2	4.3
F7	FHENFYDWFDRQVGGSGGGGFPVRTGRTVLGGFSVRLLLW	15.0	2.7	10.9	0.2	4.1
G1	SHDNFYDWFVR.VSGSGGGGSPLCVLGNCSG	11.3	2.8	10.6	0.3	3.8
E8	FYDNFYHWFDR.VSGSGGGGGSHLCVLEERVCGASLFDYRSG	13.5	0.9	3.4	0.3	3.7
E9	FSEHFYDWFARQVSGSGGGGGSHLCVLDERF.GASMVGYCSG	14.5	0.7	2.3	0.3	3.6
G2	FPENFYDWFDRQVSGSGGGGASLFG.GSG	15.3	3.8	13.1	0.3	3.5
E3	FHENFYDWFDRQVSGSSGGSHQCQVEERFWGASLCGYCSG	15.9	1.9	6.7	0.3	3.5
E12	FHDSFYDWFVRQVSGSGGGGGSHLCGLEELF.GASRFGDCSG	10.0	2.3	6.8	0.3	2.9
E5	OUT OF FRAME	14.7	3.7	9.6	0.4	2.6
F8	FHGDFYDWFVR.VSGSGGGGGSHLCVLEELYCSG	13.7	3.6	9.5	0.4	2.6
E6	FHDNFYDWFVR.VSGSGGGGGSHLCVVEERFWGGSPIGYCSG	13.3	3.0	7.3	0.4	2.5
G8	OUT OF FRAME	13.9	4.5	10.5	0.4	2.4
E1	FQDNFYDWFVRQVSGSGGGSHRCVLEGCSCG	13.4	5.8	13.3	0.4	2.3
H12	FHENFYDWFDRQVSGGSACLFGYCSG	9.8	3.9	8.5	0.5	2.2
F2	YHENFYDWFVR.VSGSGG	14.4	6.2	12.8	0.5	2.1
H6	VHESFYDWFVR.VAGSGGGGGSHLCVDVDCSG	11.5	4.8	9.6	0.5	2.0
H4	FHDNFYDWFDRQVSGSGGGGSPFG.RSD	11.2	5.3	10.0	0.5	1.9
H5	FH.HFYDWFDRQVSGSGGGGSLLCVGEPEFWGASLFAYCSG	11.8	4.4	8.5	0.5	1.9
E7	FHENFYDWFVRQVSGSGGGSGG	15.4	7.8	14.0	0.6	1.8
F5	FHESFYDWFVR.VPGSGGGGSQLCVQEELFEGDSSLGDCSG	16.8	7.3	12.9	0.6	1.8
F10		13.9	5.9	10.8	0.5	1.8
E10	FHENFYEWFDQRQVSGSGGVLDERF.GACPSGYCSG	10.6	5.1	8.9	0.6	1.8

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FIG. 44B-1

Clone	Sequence	E-Tag	IR	IGFR	IR/IGFR	IGFR/IR
F4	FHDNFYDWFVR.VAGSGSGSGSHLCVPEELFWGASLFGYC <u>CSG</u>	15.7	3.1	5.6	0.6	1.8
H2	FGEDFYDWFVR.VSGSGSGSGSHLCVLDLFWDASPFQCPG	11.4	2.5	4.6	0.6	1.8
E11	.HDNFYGFDRQVSGSGSGSGSHLCVLDLFWGASLFGYC <u>S</u>	11.7	1.3	2.2	0.6	1.7
F12	FQENFYDWFVR.VSGDELSGASQCGSCG	10.6	7.0	9.6	0.7	1.4
F9	SHESFYDWFVRQVSGSGSGSGSDLCVWEELCGGAPLVG.GSS	16.0	9.9	13.3	0.7	1.3
E4	FPENFYDWFDRQVSGSGSGSGSSG	16.4	13.4	15.8	0.8	1.2
H10	FRENFYDWFVRQVSGSGSGSGSHLCVLEELSWGASTFGSCSG	10.8	7.8	9.1	0.9	1.2
F3	IHVDFYDWFAR.VSGSGSGSGSHLCVLDLFWDASLFGDCAG	14.2	3.9	4.6	0.8	1.2
G6	FHASFYDWFDRQVSGSGSGSGSHLCVLEGLFWGAAPFGYC <u>CSG</u>	16.2	11.0	12.1	0.9	1.1
H3	SDANFYDWFRL.VSGSGSGSGSHLCVLEEQFWDASLFGDCSG	13.1	9.8	11.1	0.9	1.1
G5	FHDKFYDWFVS.VAGSGSGSGSHLCVLEDRFWGSSLSGYC <u>CSG</u>	14.7	7.1	7.9	0.9	1.1
H9	FHDNFYDWFVRQVTDGSGSGSGQLCVVEDLFWDASRFGYC.G	13.1	8.2	8.0	1.0	1.0
G3	VSEDFYEWFRV.ASGSGSGSGSHLCVLEELFWGSSSLIGDCSG	13.7	11.7	2.5	4.6	0.2
G4	FPENFYDWFVRQVSGSGSGSGSHLCVLEEL.WGASMFGYC <u>CSG</u>	10.0	4.3	0.7	6.0	0.2
F6	FQENFYDWFVRQVSGSGSGSGSHLCVLEALFWGASLFG.CSG	5.6	9.0	0.4	21.2	0.0
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Non-Binders:						
H1	DYKDGRRGRF.GRSSVVLWKRL.R	1.2	0.7	0.5	1.5	0.7
G10	DTKTFIGITGVLPRLSAV.GFWGGSW	1.7	0.3	0.3	0.8	1.2
G9	CHENFYVWFVSQVAGSGSGSGSRLCIM.ELFRGASLFGYSSG	2.0	0.4	0.5	0.9	1.1
F1	FHANFYDWFVR.VSGSGSGSGSHLCVLEELVSGPSLLGYC <u>CSG</u>	14.5	0.6	1.5	0.4	2.3
H8	FHEKFYDWFDL.LSGSGSGSGSHLCVREEPFWGASLFGYCPG	9.7	0.6	1.5	0.4	2.3

FIG. 44B-2

IGFR Binders with change in Cys

Clone	Sequence	E-Tag	IR	IGFR	IR/IGFR	IGFR/IR
F8 (X14)	HL <u>C</u> VLEELFWGASLFGY <u>C</u> SG					
D8 (X6)	WLDQEWAWVQCEVYGRG <u>C</u> PS					
G1 (X4)	SHDNFYDWFVR.VSGSGSGSGSPL <u>C</u> VLGN <u>C</u> SG	11.3	2.8	10.6	0.3	3.8
E8 (X6)	FYDNFYHWFDR.VSGSGSGSGSHL <u>C</u> VLEERVCGASLFDY <u>R</u> SG	13.5	0.9	3.4	0.3	3.7
E3 (X10)	FHENFYDWFDRQVSGSGSGSGSHQ <u>C</u> VQEERFWGASL <u>C</u> GY <u>C</u> SG	15.9	1.9	6.7	0.3	3.5
F8 (X6)	FHGDFYDWFVR.VSGSGSGSGSHL <u>C</u> VLEELY <u>C</u> SG	13.7	3.6	9.5	0.4	2.6
E1 (X4)	FQDNFYDWFVRQVSGSGSGSGSHR <u>C</u> VLEG <u>C</u> SG	13.4	5.8	13.3	0.4	2.3
H12 (X4)	FHENFYDWFDRQVSGSACLFGY <u>C</u> SG	9.8	3.9	8.5	0.5	2.2
H6 (X3)	VHESFYDWFVR.VAGSGSGSGSHL <u>C</u> DVDC <u>S</u> SG	11.5	4.8	9.6	0.5	2.0
E10 (X4)	FHENFYEWFDQRQVSGSGGVLD <u>R</u> FGACPSGY <u>C</u> SG	10.6	5.1	8.9	0.6	1.8
F12 (X2)	FQENFYDWFVR.VSGDELGGASQ <u>G</u> SGSG	10.6	7.0	9.6	0.7	1.4
F9 (X5)	SHESFYDWFVRQVSGSGSGSGSDL <u>C</u> VWEELCGGAPLVG.GSS	16.0	9.9	13.3	0.7	1.3

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IGFR Binders with loss of F8

G7	FHANFYDWFVRQV.GSGSGSGSGSG	16.1	2.1	9.8	0.2	4.7
F2	YHENFYDWFVR.VSGSGSG	14.4	6.2	12.8	0.5	2.1
E7	FHENFYDWFVRQVSGSGSGSGG	15.4	7.8	14.0	0.6	1.8
E4	FPENFYDWFDRQVSGSGSGSGSGSG	16.4	13.4	15.8	0.8	1.2

IGFR Binders with loss of Cys in F8

F11	FHENFYDWFVRQVSGSGSGSGSHL.GSG	12.5	0.8	5.2	0.2	6.5
H7	.HENFYDWFVRQLSGSGSGSDGSHLFGY <u>G</u> SG	7.2	0.6	2.7	0.2	4.5
F7	FHENFYDWFDRQVSGSGSGSGSFVRTGRITVLGGFSVRLLW	15.0	2.7	10.9	0.2	4.1
G2	FPENFYDWFDRQVSGSGSGGASLFG.GSG	15.3	3.8	13.1	0.3	3.5
H4	FHDNFYDWFDRQVSGSGSGSGSPFG.RSD	11.2	5.3	10.0	0.5	1.9

FIG. 44B-3

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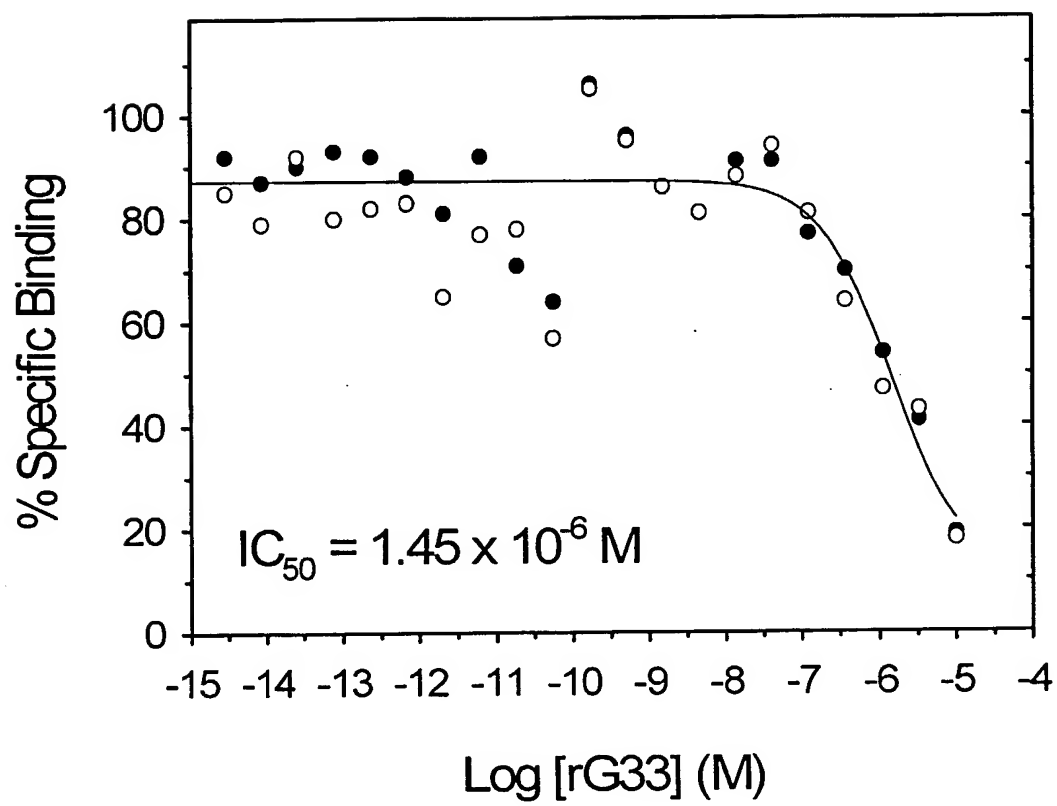


FIG. 45

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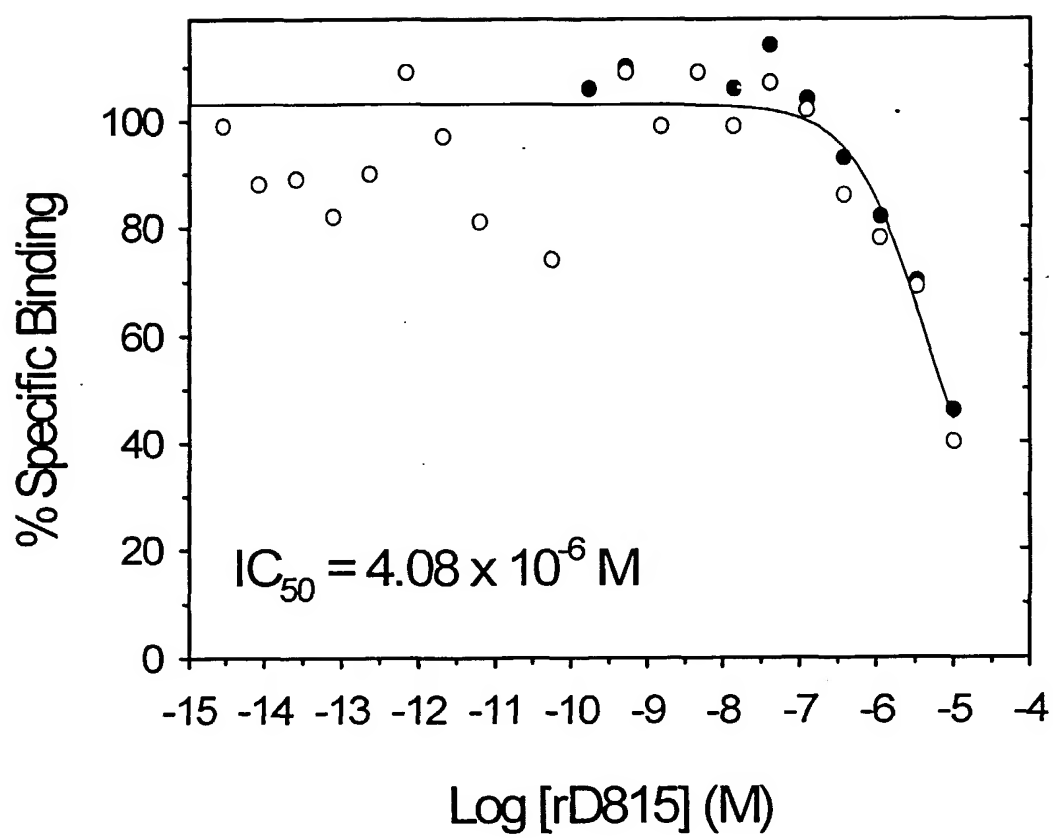


FIG. 46

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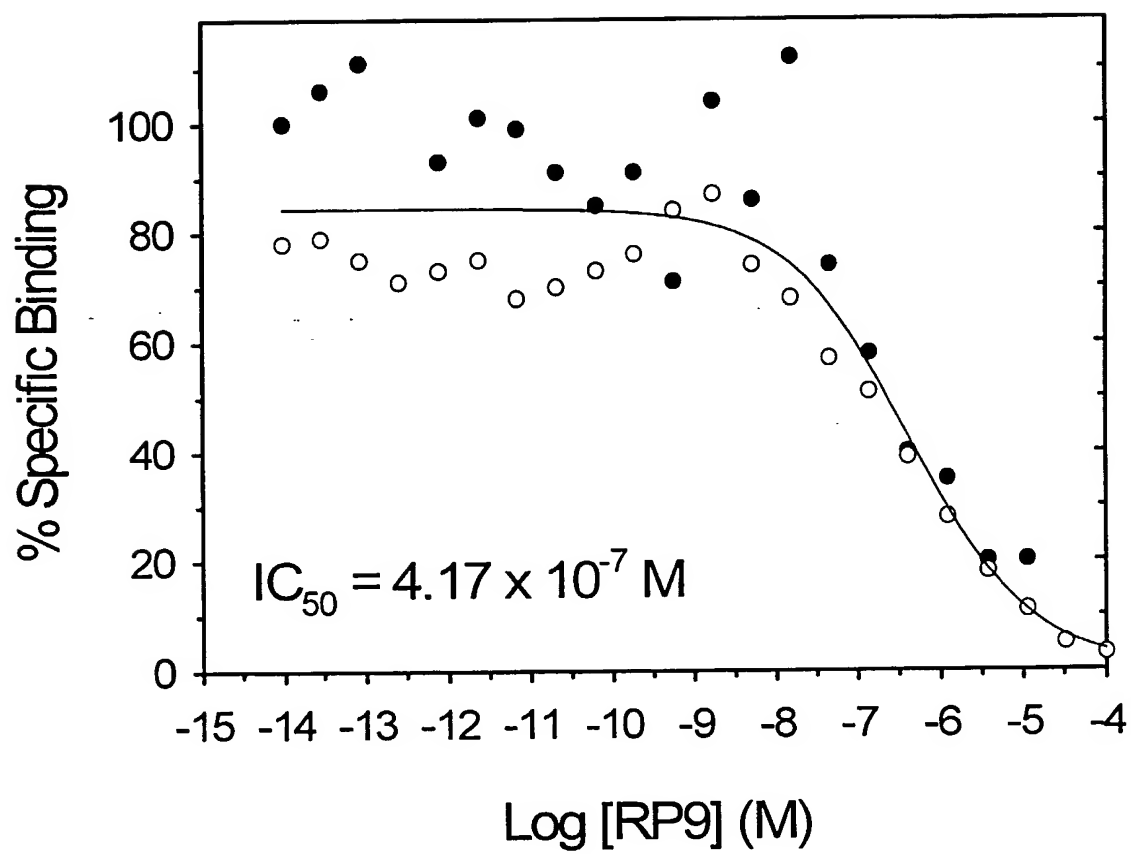


FIG. 47

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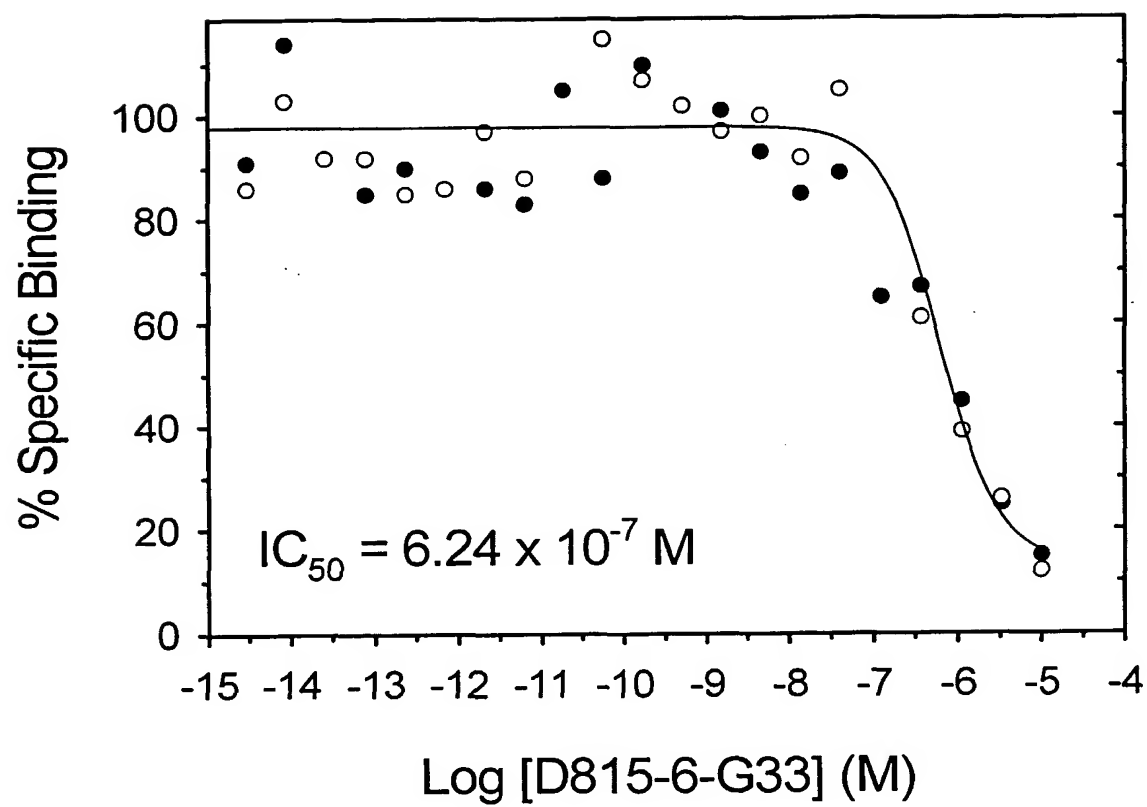


FIG. 48

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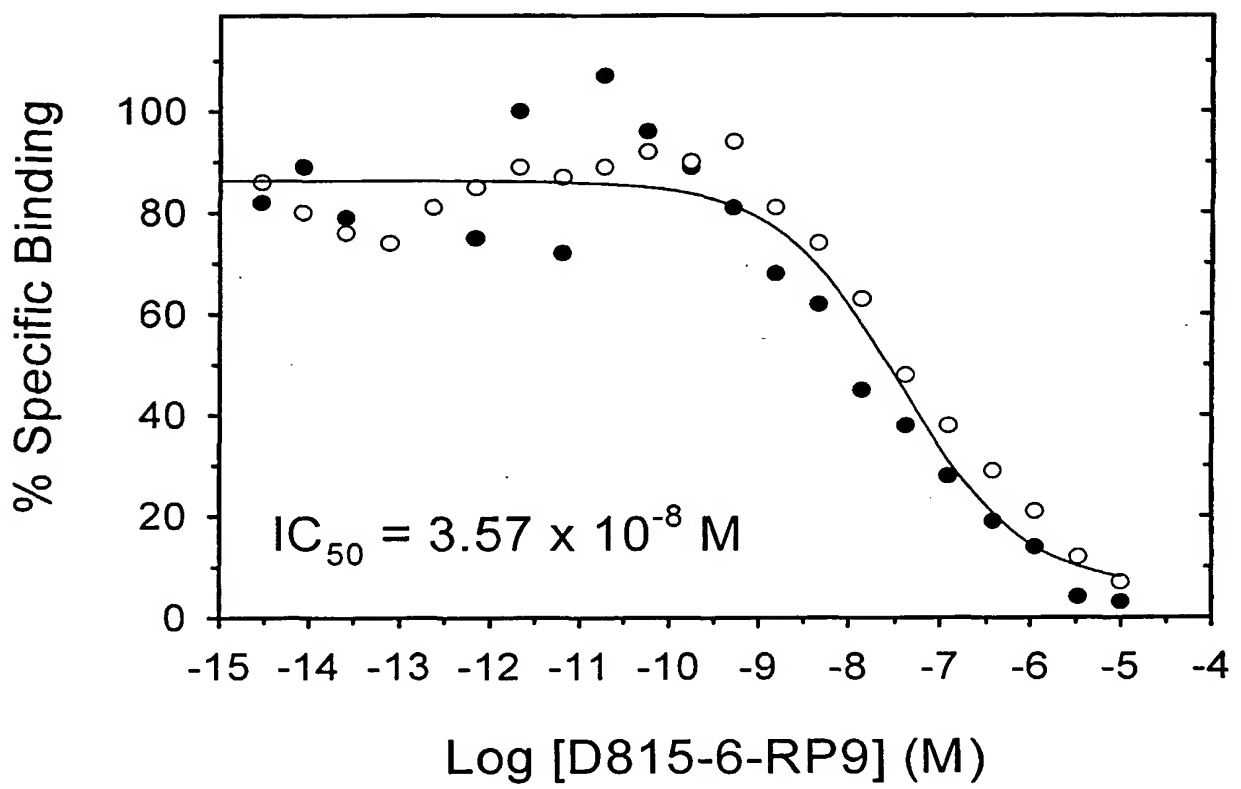


FIG. 49

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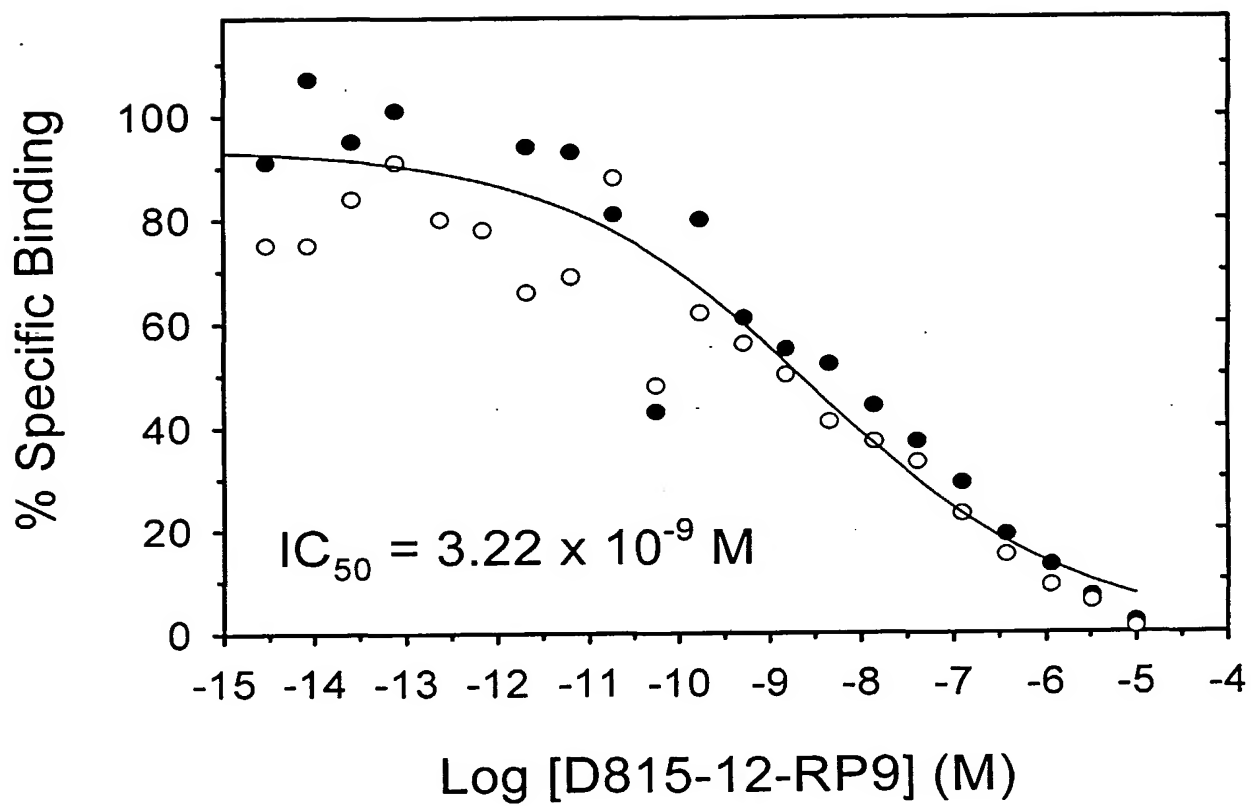


FIG. 50

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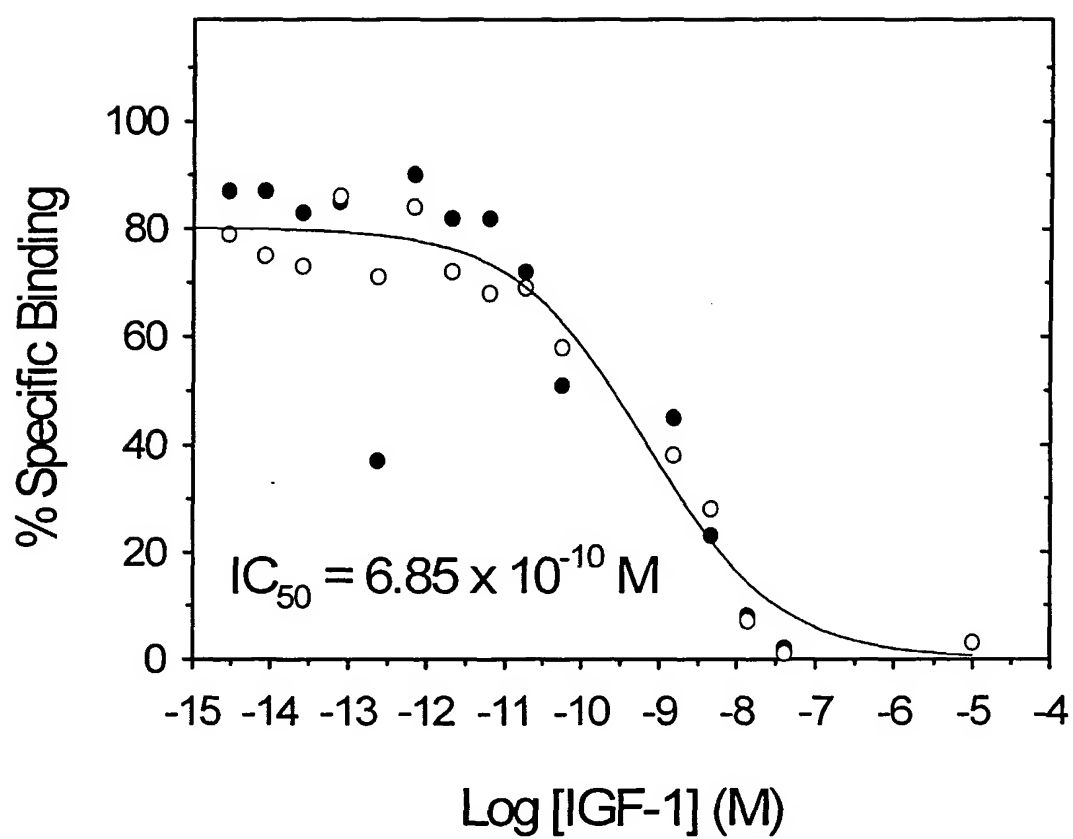


FIG. 51

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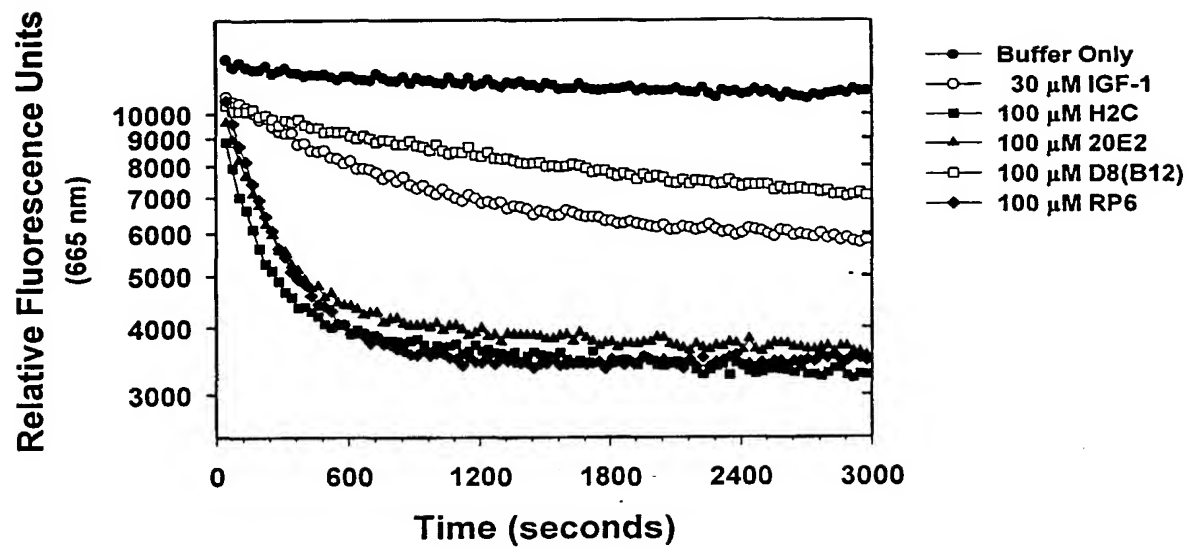


FIG. 52

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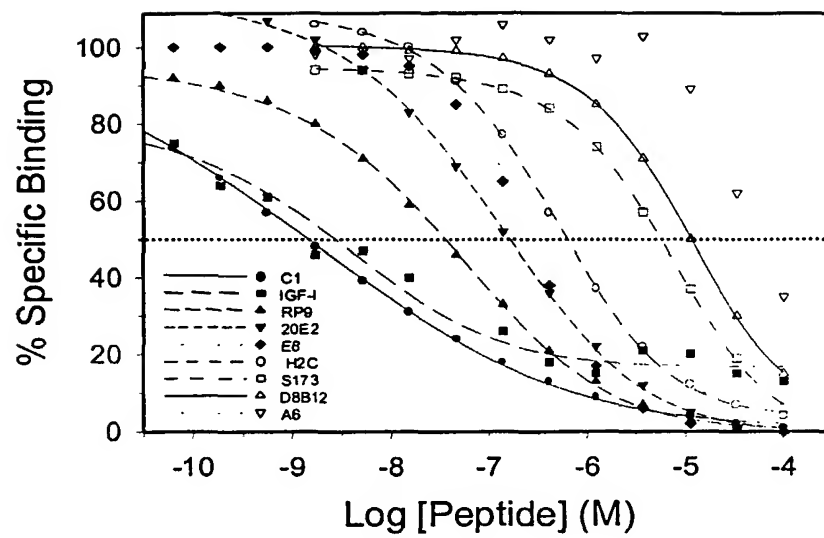
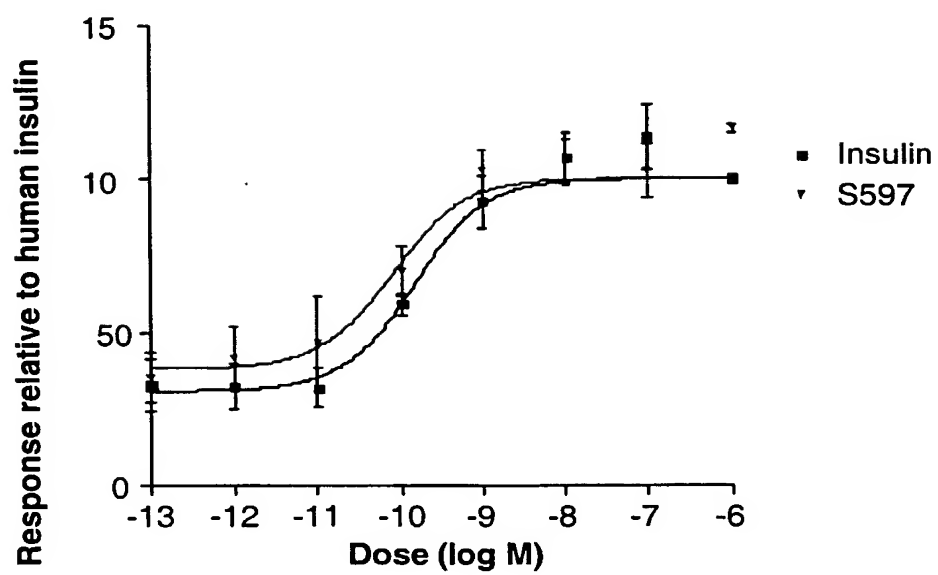


FIG. 53

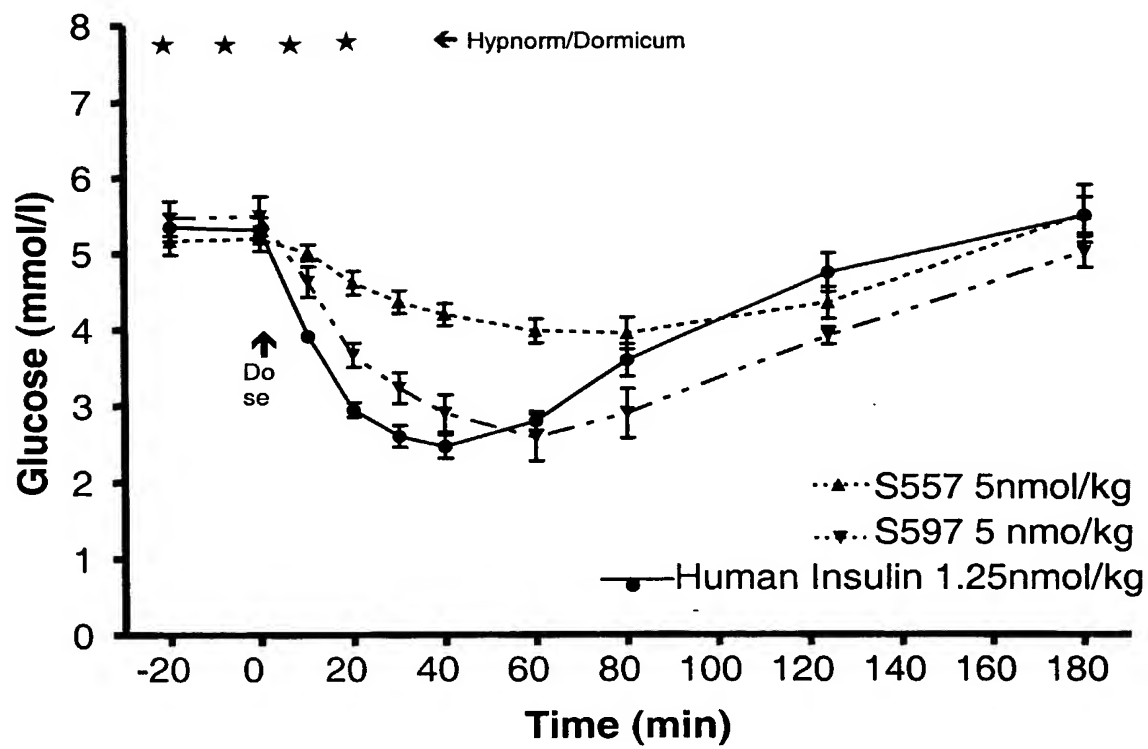
Figure 54:

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Figure 55:



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Figure 56:

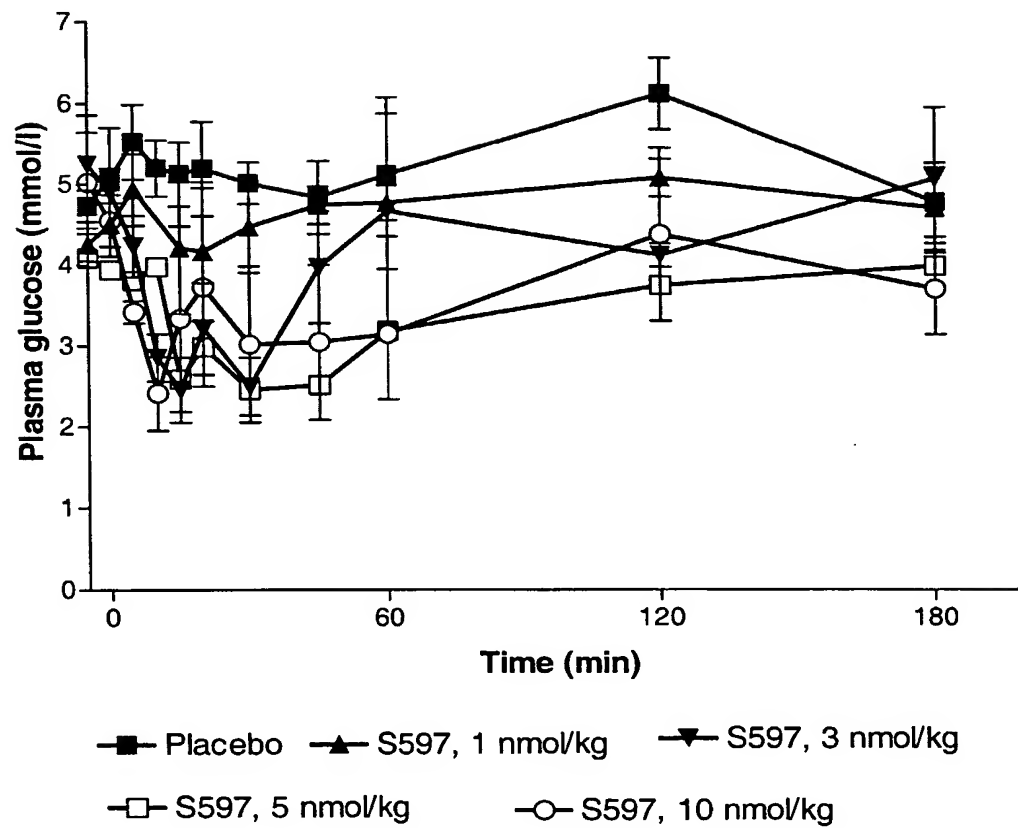


Figure 57

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